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OM protein - protein search, using sw model

Run on: September 5, 2006, 20:21:18 ; Search time 35 Seconds
(without alignments)
1334.167 Million cell updates/sec

Perfect score: 3502
Sequence: 1 MRYVLTMKASVIMFLVL.....QYVRIQICTEPNSOPRN 678

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
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Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3502	100.0	678	US-11-101-316-34	Sequence 34, Appl
3	3502	100.0	678	US-11-376-673-34	Sequence 34, Appl
5	471.5	13.5	3176	US-11-105-233-155	Sequence 15, Appl
6	357.5	10.2	956	US-10-527-101-8	Sequence 8, Appl
7	325.5	9.3	755	US-11-274-634-14	Sequence 14, Appl
8	324.5	9.3	732	US-11-274-634-14	Sequence 14, Appl
9	282.5	8.1	488	US-11-274-634-14	Sequence 3, Appl
10	270.5	7.7	2804	US-10-541-708-68	Sequence 21, Appl
11	266	7.6	2813	US-11-222-346A-7	Sequence 48, Appl
12	232	6.6	1152	US-09-970-076-3	Sequence 21, Appl
13	231	6.6	1152	US-10-511-937-2444	Sequence 3, Appl
14	227.5	6.5	445	US-10-530-187-280	Sequence 2444, Appl
15	204.5	5.8	436	US-10-505-928-892	Sequence 280, Appl
16	203.5	5.8	1170	US-10-511-937-8007	Sequence 532, Appl
17	193	5.5	1151	US-11-246-999-103	Sequence 3007, Appl
18	192.5	5.5	1034	US-11-246-999-43	Sequence 103, Appl
19	192.5	5.5	1146	US-11-175-714-150	Sequence 43, Appl
20	192.5	5.5	1146	US-11-175-714-148	Sequence 150, Appl
21	192.5	5.5	1188	US-11-175-714-147	Sequence 148, Appl
22	192.5	5.5	1189	US-11-246-999-35	Sequence 147, Appl
23	191.5	5.5	1141	US-11-175-714-168	Sequence 35, Appl
24	191.5	5.5	1166	US-11-175-714-166	Sequence 168, Appl
25	191.5	5.5	1188	US-11-175-714-165	Sequence 165, Appl
26	190.5	5.4	437	US-11-293-697-3386	Sequence 165, Appl
27	172	4.9	182	US-11-175-714-151	Sequence 3386, Appl
28	171	4.9	182	US-11-175-714-159	Sequence 151, Appl

29	171	4.9	734	US-11-165-586-45	Sequence 45, Appl
30	170.5	4.9	198	US-09-970-076-4	Sequence 4, Appl
31	163.5	4.7	765	US-11-165-586-36	Sequence 36, Appl
32	155.5	4.4	769	US-11-165-586-27	Sequence 27, Appl
33	149.5	4.3	1132	US-11-347-179-5	Sequence 5, Appl
34	149.5	4.3	1167	US-11-175-714-162	Sequence 162, Appl
35	149.5	4.3	1167	US-11-347-179-4	Sequence 4, Appl
37	134.5	3.8	485	US-11-056-3558-12397	Sequence 12397, A
38	133.5	3.8	213	US-11-222-346A-4	Sequence 4, Appl
39	133.5	3.8	524	US-11-293-697-3442	Sequence 3442, Ap
40	131.5	3.8	246	US-11-222-346A-5	Sequence 5, Appl
41	131.5	3.8	247	US-11-350-353-4	Sequence 4, Appl
42	127	3.6	419	US-11-056-3558-45520	Sequence 45520, A
43	119.5	3.4	213	US-11-222-346A-6	Sequence 6, Appl
44	119.5	3.4	22152	US-10-544-944-1	Sequence 1, Appl
45	116.5	3.3	2186	US-10-471-571A-860	Sequence 860, Appl
46	115	3.3	375	US-11-056-3558-45521	Sequence 45521, A
47	114	3.3	571	US-10-449-902-42330	Sequence 42330, A
48	113.5	3.2	405	US-10-953-349-1810	Sequence 1810, Ap
49	113.5	3.2	413	US-10-953-349-1809	Sequence 1809, Ap
50	113.5	3.2	422	US-10-953-349-1808	Sequence 1808, Ap
51	113.5	3.2	480	US-10-374-780A-2902	Sequence 2902, Ap
52	112.5	3.2	748	US-10-449-902-42316	Sequence 42316, A
53	112	3.2	231	US-11-293-697-4167	Sequence 4167, Ap
54	111.5	3.2	382	US-10-953-349-24980	Sequence 24980, A
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59	110	3.1	478	US-11-056-3558-78732	Sequence 78732, A
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63	108.5	3.1	384	US-10-449-902-41009	Sequence 41009, A
64	108.5	3.1	681	US-10-953-349-10919	Sequence 10919, A
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66	108.5	3.1	681	US-11-056-3558-49007	Sequence 49007, A
67	108	3.1	422	US-10-953-349-26025	Sequence 26025, A
68	108	3.1	422	US-11-056-3558-63446	Sequence 63446, A
69	107.5	3.1	666	US-10-449-902-45827	Sequence 45827, A
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71	107.5	3.1	1058	US-10-449-902-31441	Sequence 31441, A
72	107	3.1	880	US-10-953-349-6391	Sequence 6391, Ap
73	106.5	3.0	347	US-11-056-3558-45522	Sequence 45522, A
74	106	3.0	1055	US-10-449-902-41244	Sequence 41244, A
75	105.5	3.0	684	US-10-449-902-45113	Sequence 45113, A
76	105	3.0	354	US-10-953-349-28519	Sequence 28519, A
77	105	3.0	354	US-11-056-3558-65407	Sequence 65407, A
78	104.5	3.0	2801	US-10-540-898-630	Sequence 630, Appl
79	104	3.0	493	US-11-056-3558-65494	Sequence 65494, A
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81	103.5	3.0	563	US-11-174-1078-4904	Sequence 4904, Ap
82	103.5	3.0	577	US-11-293-697-3929	Sequence 3929, Ap
83	103.5	3.0	654	US-11-192-046-231	Sequence 231, Appl
84	103	2.9	334	US-11-293-697-2527	Sequence 2527, Ap
85	103	2.9	474	US-11-056-3558-72370	Sequence 72370, A
86	102.5	2.9	348	US-11-056-3558-8475	Sequence 8475, Ap
87	102.5	2.9	348	US-11-056-3558-13644	Sequence 13644, A
88	102.5	2.9	843	US-11-043-842-489	Sequence 489, Appl
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104	102.5	2.9	1685	7	US-11-043-842-497	Sequence 497, App	177	97	2.8	512	7	US-11-056-3558-12249	Sequence 12249, A
105	102.5	2.9	1691	7	US-11-043-842-500	Sequence 500, App	178	97	2.8	587	7	US-11-293-697-3807	Sequence 3807, Ap
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107	102.5	2.9	1744	7	US-11-043-842-485	Sequence 485, App	180	97	2.8	897	7	US-11-330-403-2599	Sequence 2599, Ap
108	102.5	2.9	1744	7	US-11-043-842-486	Sequence 486, App	181	97	2.8	892	6	US-10-449-902-47486	Sequence 47486, A
109	102.5	2.9	1744	7	US-11-043-842-487	Sequence 487, App	182	97	2.8	233	6	US-10-953-349-31470	Sequence 31470, A
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111	102	2.9	432	6	US-10-449-902-56608	Sequence 56608, A	184	96.5	2.8	334	7	US-11-056-3558-12828	Sequence 16288, A
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113	102	2.9	652	6	US-10-953-349-5551	Sequence 5551, Ap	186	96.5	2.8	513	7	US-11-330-403-11599	Sequence 11599, A
114	102	2.9	652	7	US-11-056-3558-30482	Sequence 30482, A	187	96.5	2.8	624	6	US-10-449-902-54592	Sequence 54592, A
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116	102	2.9	652	7	US-11-056-3558-97017	Sequence 97017, A	189	96.5	2.8	733	7	US-11-056-3558-42029	Sequence 42029, A
117	102	2.9	693	7	US-11-293-697-3849	Sequence 3849, Ap	190	96.5	2.8	733	7	US-11-056-3558-49630	Sequence 49630, A
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121	101	2.9	326	7	US-11-056-3558-53421	Sequence 53421, A	194	96.5	2.8	861	6	US-10-953-349-11809	Sequence 11809, A
122	101	2.9	343	6	US-10-953-349-17337	Sequence 17337, A	195	96.5	2.8	887	6	US-10-953-349-11808	Sequence 11808, A
123	101	2.9	343	6	US-11-056-3558-53420	Sequence 53420, A	196	96.5	2.8	1004	6	US-10-953-349-11807	Sequence 11807, A
124	101	2.9	350	6	US-10-953-349-17336	Sequence 17336, A	197	96	2.7	332	7	US-11-330-403-31432	Sequence 31432, Ap
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135	100	2.9	564	1	US-09-970-076-6	Sequence 6, Appl1	208	96	2.7	1601	6	US-10-539-228-225	Sequence 225, App
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139	99.5	2.8	411	6	US-10-449-902-8078	Sequence 8078, A	212	95.5	2.7	443	6	US-10-449-902-28738	Sequence 28738, A
140	99.5	2.8	915	6	US-10-523-014-4	Sequence 4, Appl1	213	95.5	2.7	512	7	US-11-056-3558-12932	Sequence 12032, A
141	99	2.8	335	6	US-10-953-349-52526	Sequence 25256, A	214	95.5	2.7	782	6	US-10-539-228-438	Sequence 438, App
142	99	2.8	338	6	US-10-953-349-4981	Sequence 24981, A	215	95.5	2.7	1217	7	US-11-105-233-186	Sequence 186, App
143	99	2.8	338	7	US-11-056-3558-54474	Sequence 54474, A	216	95	2.7	282	7	US-11-056-3558-55443	Sequence 5643, Ap
144	99	2.8	384	6	US-10-505-928-395	Sequence 395, App	217	95	2.7	654	6	US-10-480-962-9	Sequence 9, Appl1
145	99	2.8	535	6	US-10-449-902-45610	Sequence 45610, A	218	95	2.7	766	6	US-10-527-572-6	Sequence 6, Appl1
146	99	2.8	632	7	US-11-056-3558-45762	Sequence 45762, A	219	95	2.7	2829	6	US-10-525-621-1	Sequence 1, Appl1
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148	99	2.8	759	6	US-10-449-902-41321	Sequence 41321, A	221	94.5	2.7	447	7	US-11-056-3558-113532	Sequence 113532, A
149	99	2.8	856	6	US-10-449-902-41385	Sequence 41385, A	222	94.5	2.7	513	7	US-11-330-403-5559	Sequence 5559, Ap
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174	97.5	2.8	1434	7	US-11-192-046-36	Sequence 36, Appl1	247	94	2.7	368	7	US-11-056-3558-63447	Sequence 63447, A
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251	93.5	2.7	514	6	US-10-449-902-50931	Sequence 50931, A	324	91	2.6	380	7	US-11-056-3558-2695	Sequence 2695, Ap
252	93.5	2.7	548	6	US-10-449-902-29496	Sequence 29496, A	325	91	2.6	488	7	US-11-330-403-18128	Sequence 18128, A
253	93.5	2.7	585	6	US-10-449-902-53167	Sequence 53167, A	326	91	2.6	626	7	US-11-358-419-4813	Sequence 43, Appl
254	93.5	2.7	595	7	US-11-056-3558-83512	Sequence 83512, A	327	91	2.6	626	7	US-11-378-923-23	Sequence 23, Appl
255	93.5	2.7	598	7	US-11-056-3558-83511	Sequence 83511, A	328	91	2.6	626	7	US-11-378-923-24	Sequence 24, Appl
256	93.5	2.7	617	6	US-10-449-902-36554	Sequence 36554, A	329	91	2.6	698	7	US-11-056-3558-79590	Sequence 79590, A
257	93.5	2.7	764	6	US-10-449-902-46298	Sequence 46298, A	330	91	2.6	712	7	US-10-449-902-53993	Sequence 53993, A
258	93.5	2.7	905	6	US-10-449-902-41605	Sequence 41605, A	331	91	2.6	712	7	US-11-105-233-162	Sequence 162, App
259	93.5	2.7	918	7	US-11-056-3558-78339	Sequence 78339, A	332	91	2.6	712	7	US-11-121-133-262	Sequence 262, App
260	93.5	2.7	1127	6	US-10-449-902-53809	Sequence 53809, A	333	91	2.6	712	7	US-11-121-133-263	Sequence 263, App
261	93.5	2.7	2240	6	US-10-544-731-4	Sequence 4, Appl1	334	91	2.6	712	7	US-11-121-133-264	Sequence 264, App
262	93.5	2.7	2258	6	US-10-544-731-3	Sequence 3, Appl1	335	91	2.6	718	7	US-11-056-3558-79589	Sequence 79589, A
263	93.5	2.7	2264	6	US-10-544-731-5	Sequence 5, Appl1	336	91	2.6	847	7	US-11-056-3558-73588	Sequence 73588, A
264	93	2.7	251	6	US-10-953-349-9196	Sequence 9196, Ap	337	91	2.6	883	7	US-11-192-046-188	Sequence 188, App
265	93	2.7	251	7	US-11-056-3558-39265	Sequence 39265, A	338	91	2.6	883	7	US-11-192-046-195	Sequence 195, App
266	93	2.7	251	7	US-11-056-3558-41773	Sequence 41773, A	339	91	2.6	883	7	US-11-192-046-202	Sequence 202, App
267	93	2.7	302	6	US-10-953-349-9195	Sequence 9195, Ap	340	91	2.6	883	7	US-11-192-046-216	Sequence 216, App
268	93	2.7	302	6	US-11-056-3558-39264	Sequence 39264, A	341	91	2.6	883	7	US-11-192-046-237	Sequence 237, App
269	93	2.7	302	7	US-11-056-3558-41772	Sequence 41772, A	342	91	2.6	883	7	US-11-192-046-173	Sequence 173, App
270	93	2.7	326	6	US-10-953-349-9194	Sequence 9194, Ap	343	91	2.6	1226	7	US-11-221-332-88	Sequence 88, Appl
271	93	2.7	326	7	US-11-056-3558-39263	Sequence 39263, A	344	90.5	2.6	1226	7	US-11-056-3558-113708	Sequence 13208, A
272	93	2.7	326	7	US-11-056-3558-41771	Sequence 41771, A	345	90.5	2.6	288	6	US-10-449-902-33415	Sequence 33415, A
273	93	2.7	361	7	US-11-056-3558-1150	Sequence 1150, Ap	346	90.5	2.6	492	6	US-10-449-902-42619	Sequence 42619, A
274	93	2.7	381	7	US-11-056-3558-1149	Sequence 1149, Ap	347	90.5	2.6	500	7	US-11-330-403-13209	Sequence 13209, A
275	93	2.7	594	6	US-10-449-902-47022	Sequence 47022, A	348	90.5	2.6	501	6	US-10-449-902-47505	Sequence 47505, A
276	93	2.7	594	6	US-10-449-902-52090	Sequence 52090, A	349	90.5	2.6	521	6	US-10-449-902-54672	Sequence 54672, A
277	93	2.7	627	7	US-11-358-419-47	Sequence 47, Appl	350	90.5	2.6	570	6	US-10-449-902-51709	Sequence 51709, A
278	93	2.7	657	6	US-10-449-902-41222	Sequence 41222, A	351	90.5	2.6	579	6	US-10-449-902-52147	Sequence 52147, A
279	93	2.7	879	6	US-10-540-898-258	Sequence 258, App	352	90.5	2.6	627	6	US-10-449-902-45436	Sequence 45436, A
280	93	2.7	901	6	US-10-540-898-870	Sequence 870, App	353	90.5	2.6	634	6	US-10-449-902-55716	Sequence 55716, A
281	93	2.7	1786	6	US-10-519-328-2	Sequence 2, Appl1	354	90.5	2.6	710	6	US-10-449-902-41319	Sequence 41319, A
282	93	2.7	1821	6	US-10-505-928-451	Sequence 451, App	355	90.5	2.6	727	6	US-10-449-902-53529	Sequence 53529, A
283	93	2.7	1821	6	US-10-519-328-1	Sequence 1, Appl1	356	90.5	2.6	866	6	US-10-449-902-41251	Sequence 41251, A
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285	92.5	2.6	334	6	US-10-449-902-40166	Sequence 40166, A	358	90.5	2.6	882	6	US-10-977-350-4	Sequence 4, Appl1
286	92.5	2.6	334	6	US-11-349-852-7	Sequence 7, Appl1	359	90.5	2.6	939	6	US-10-449-902-41088	Sequence 41088, A
287	92.5	2.6	342	6	US-10-449-902-49563	Sequence 49563, A	360	90.5	2.6	1073	6	US-10-449-902-41088	Sequence 41088, A
288	92.5	2.6	359	7	US-11-349-852-8	Sequence 8, Appl1	361	90.5	2.6	1122	6	US-10-540-898-260	Sequence 260, App
289	92.5	2.6	364	6	US-10-505-928-605	Sequence 605, Appl1	362	90.5	2.6	1433	7	US-11-330-403-8279	Sequence 8279, Ap
290	92.5	2.6	382	7	US-11-293-687-654	Sequence 654, App	363	90.5	2.6	1572	7	US-11-330-403-12338	Sequence 12338, A
291	92.5	2.6	505	7	US-11-330-403-18387	Sequence 18387, A	364	90	2.6	302	7	US-11-056-3558-8476	Sequence 8476, Ap
292	92.5	2.6	590	6	US-10-449-902-55352	Sequence 55352, A	365	90	2.6	302	7	US-11-056-3558-15645	Sequence 13645, A
293	92.5	2.6	860	7	US-11-293-431-3	Sequence 3, Appl1	366	90	2.6	302	7	US-11-056-3558-16284	Sequence 16284, A
294	92.5	2.6	901	7	US-11-293-697-2845	Sequence 2845, Ap	367	90	2.6	317	6	US-10-953-349-17089	Sequence 17089, A
295	92.5	2.6	1017	6	US-10-449-902-41143	Sequence 41143, A	368	90	2.6	339	6	US-10-953-349-17088	Sequence 17088, A
296	92.5	2.6	2828	6	US-10-700-439-124	Sequence 124, App	369	90	2.6	347	6	US-10-953-349-17087	Sequence 17087, A
297	92	2.6	245	6	US-10-449-902-38546	Sequence 38546, A	370	90	2.6	412	7	US-11-056-3558-8069	Sequence 8069, Ap
298	92	2.6	315	7	US-11-056-3558-63975	Sequence 63975, A	371	90	2.6	557	6	US-10-449-902-28939	Sequence 28939, A
299	92	2.6	427	6	US-10-449-902-53158	Sequence 53158, A	372	90	2.6	587	7	US-11-056-3558-107995	Sequence 107995, A
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301	92	2.6	591	6	US-10-953-349-5074	Sequence 5074, Ap	374	90	2.6	719	7	US-11-056-3558-117994	Sequence 117994, A
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304	92	2.6	675	6	US-10-449-902-88447	Sequence 88447, A	377	90	2.6	877	7	US-11-056-3558-44815	Sequence 44815, A
305	92	2.6	709	6	US-10-449-902-52735	Sequence 52735, A	378	90	2.6	885	7	US-11-056-3558-39834	Sequence 39834, A
306	92	2.6	712	6	US-10-530-187-896	Sequence 286, App	379	90	2.6	885	7	US-11-056-3558-44814	Sequence 44814, A
307	92	2.6	1123	7	US-11-330-403-11476	Sequence 11476, A	380	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
308	92	2.6	1123	7	US-11-330-403-15911	Sequence 15911, A	381	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
309	92	2.6	1124	7	US-11-330-403-15911	Sequence 15911, A	382	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
310	92	2.6	1135	7	US-11-301-457-21	Sequence 21, Appl1	383	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
311	92	2.6	1581	7	US-11-283-329-162	Sequence 162, App	384	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
312	91.5	2.6	317	7	US-11-056-3558-68675	Sequence 68675, A	385	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
313	91.5	2.6	359	7	US-11-056-3558-68674	Sequence 68674, A	386	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
314	91.5	2.6	359	7	US-11-330-403-1146	Sequence 3146, Ap	387	90	2.6	1123	7	US-11-330-403-17447	Sequence 17347, A
315	91.5	2.6	423	7	US-11-056-3558-68673	Sequence 68673, A	388	90	2.6	1123	7	US-11-330-403-17447	Sequence 17347, A
316	91.5	2.6	718	7	US-11-056-3558-79095	Sequence 79095, A	389	89.5	2.6	310	6	US-10-953-349-24982	Sequence 24982, A
317	91.5	2.6	940	6	US-10-449-902-14146	Sequence 14146, A	390	89.5	2.6	310	6	US-10-953-349-24982	Sequence 24982, A
318	91.5	2.6	957	7	US-11-330-403-9644	Sequence 9644, Ap	391	89.5	2.6	317	7	US-11-056-3558-50674	Sequence 50674, A
319	91	2.6	214	6	US-10-449-902-55454	Sequence 55454, A	392	89.5	2.6	434	6	US-10-449-902-50843	Sequence 50843, A
320	91	2.6	251	6	US-11-284-236-212	Sequence 212, App	393	89.5	2.6	438	6	US-10-953-349-11578	Sequence 11578, A
321	91	2.6	344	7	US-11-121-133-173	Sequence 173, App	394	89.5	2.6	438	7	US-11-056-3558-48934	Sequence 48934, A

395	89.5	2.6	440	6	US-10-953-349-11277	Sequence 11277, A	468	89.5	2.6	499	7	US-11-241-596-230	Sequence 230, App
396	89.5	2.6	440	7	US-11-056-355B-48933	Sequence 48933, A	469	89.5	2.6	499	7	US-11-241-596-231	Sequence 231, App
397	89.5	2.6	499	7	US-11-241-596-159	Sequence 159, App	470	89.5	2.6	499	7	US-11-241-596-232	Sequence 232, App
398	89.5	2.6	499	7	US-11-241-596-160	Sequence 160, App	471	89.5	2.6	499	7	US-11-241-596-233	Sequence 233, App
399	89.5	2.6	499	7	US-11-241-596-161	Sequence 161, App	472	89.5	2.6	499	7	US-11-241-596-234	Sequence 234, App
400	89.5	2.6	499	7	US-11-241-596-162	Sequence 162, App	473	89.5	2.6	499	7	US-11-241-596-235	Sequence 235, App
401	89.5	2.6	499	7	US-11-241-596-163	Sequence 163, App	474	89.5	2.6	499	7	US-11-241-596-236	Sequence 236, App
402	89.5	2.6	499	7	US-11-241-596-164	Sequence 164, App	475	89.5	2.6	499	7	US-11-241-596-237	Sequence 237, App
403	89.5	2.6	499	7	US-11-241-596-165	Sequence 165, App	476	89.5	2.6	499	7	US-11-241-596-238	Sequence 238, App
404	89.5	2.6	499	7	US-11-241-596-166	Sequence 166, App	477	89.5	2.6	499	7	US-11-241-596-239	Sequence 239, App
405	89.5	2.6	499	7	US-11-241-596-167	Sequence 167, App	478	89.5	2.6	499	7	US-11-241-596-240	Sequence 240, App
406	89.5	2.6	499	7	US-11-241-596-168	Sequence 168, App	479	89.5	2.6	499	7	US-11-241-596-241	Sequence 241, App
407	89.5	2.6	499	7	US-11-241-596-169	Sequence 169, App	480	89.5	2.6	499	7	US-11-241-596-242	Sequence 242, App
408	89.5	2.6	499	7	US-11-241-596-170	Sequence 170, App	481	89.5	2.6	499	7	US-11-241-596-243	Sequence 243, App
409	89.5	2.6	499	7	US-11-241-596-171	Sequence 171, App	482	89.5	2.6	499	7	US-11-241-596-244	Sequence 244, App
410	89.5	2.6	499	7	US-11-241-596-172	Sequence 172, App	483	89.5	2.6	499	7	US-11-241-596-245	Sequence 245, App
411	89.5	2.6	499	7	US-11-241-596-173	Sequence 173, App	484	89.5	2.6	499	7	US-11-241-596-246	Sequence 246, App
412	89.5	2.6	499	7	US-11-241-596-174	Sequence 174, App	485	89.5	2.6	499	7	US-11-241-596-247	Sequence 247, App
413	89.5	2.6	499	7	US-11-241-596-175	Sequence 175, App	486	89.5	2.6	499	7	US-11-241-596-248	Sequence 248, App
414	89.5	2.6	499	7	US-11-241-596-176	Sequence 176, App	487	89.5	2.6	499	7	US-11-241-596-249	Sequence 249, App
415	89.5	2.6	499	7	US-11-241-596-177	Sequence 177, App	488	89.5	2.6	499	7	US-11-241-596-250	Sequence 250, App
416	89.5	2.6	499	7	US-11-241-596-178	Sequence 178, App	489	89.5	2.6	499	7	US-11-241-596-251	Sequence 251, App
417	89.5	2.6	499	7	US-11-241-596-179	Sequence 179, App	490	89.5	2.6	499	7	US-11-241-596-252	Sequence 252, App
418	89.5	2.6	499	7	US-11-241-596-180	Sequence 180, App	491	89.5	2.6	499	7	US-11-241-596-253	Sequence 253, App
419	89.5	2.6	499	7	US-11-241-596-181	Sequence 181, App	492	89.5	2.6	499	7	US-11-241-596-254	Sequence 254, App
420	89.5	2.6	499	7	US-11-241-596-182	Sequence 182, App	493	89.5	2.6	501	6	US-10-449-902-33237	Sequence 33237, A
421	89.5	2.6	499	7	US-11-241-596-183	Sequence 183, App	494	89.5	2.6	502	6	US-10-449-902-336747	Sequence 336747, A
422	89.5	2.6	499	7	US-11-241-596-184	Sequence 184, App	495	89.5	2.6	509	6	US-10-953-349-24078	Sequence 24078, A
423	89.5	2.6	499	7	US-11-241-596-185	Sequence 185, App	496	89.5	2.6	509	6	US-11-056-355B-57991	Sequence 57991, A
424	89.5	2.6	499	7	US-11-241-596-186	Sequence 186, App	497	89.5	2.6	516	6	US-10-953-349-24077	Sequence 24077, A
425	89.5	2.6	499	7	US-11-241-596-187	Sequence 187, App	498	89.5	2.6	516	6	US-10-953-355B-57990	Sequence 57990, A
426	89.5	2.6	499	7	US-11-241-596-188	Sequence 188, App	499	89.5	2.6	521	6	US-10-449-902-48426	Sequence 48426, A
427	89.5	2.6	499	7	US-11-241-596-189	Sequence 189, App	500	89.5	2.6	571	6	US-10-953-349-11276	Sequence 11276, A
428	89.5	2.6	499	7	US-11-241-596-190	Sequence 190, App	501	89.5	2.6	571	6	US-11-056-355B-44932	Sequence 44932, A
429	89.5	2.6	499	7	US-11-241-596-191	Sequence 191, App	502	89.5	2.6	594	7	US-11-330-403-1851	Sequence 1851, App
430	89.5	2.6	499	7	US-11-241-596-192	Sequence 192, App	503	89.5	2.6	643	6	US-10-505-928-249	Sequence 249, App
431	89.5	2.6	499	7	US-11-241-596-193	Sequence 193, App	504	89.5	2.6	677	7	US-11-293-697-4521	Sequence 4521, App
432	89.5	2.6	499	7	US-11-241-596-194	Sequence 194, App	505	89.5	2.6	758	6	US-10-449-902-47933	Sequence 47933, A
433	89.5	2.6	499	7	US-11-241-596-195	Sequence 195, App	507	89.5	2.6	1058	7	US-11-221-332-78	Sequence 332, App1
434	89.5	2.6	499	7	US-11-241-596-196	Sequence 196, App	508	89.5	2.6	1105	6	US-10-449-902-41991	Sequence 419, App1
435	89.5	2.6	499	7	US-11-241-596-197	Sequence 197, App	509	89.5	2.6	1105	6	US-10-449-902-41991	Sequence 419, App1
436	89.5	2.6	499	7	US-11-241-596-198	Sequence 198, App	510	89.5	2.6	1215	6	US-10-505-928-75	Sequence 75, App1
437	89.5	2.6	499	7	US-11-241-596-199	Sequence 199, App	511	89.5	2.6	1734	6	US-11-358-419-81	Sequence 81, App1
438	89.5	2.6	499	7	US-11-241-596-200	Sequence 200, App	512	89.5	2.6	1763	6	US-10-504-120-21	Sequence 21, App1
439	89.5	2.6	499	7	US-11-241-596-201	Sequence 201, App	513	89.5	2.6	1807	6	US-10-504-120-22	Sequence 22, App1
440	89.5	2.6	499	7	US-11-241-596-202	Sequence 202, App	514	89.5	2.6	227	6	US-10-953-349-32122	Sequence 32122, A
441	89.5	2.6	499	7	US-11-241-596-203	Sequence 203, App	515	89.5	2.5	242	6	US-10-953-349-34822	Sequence 34822, A
442	89.5	2.6	499	7	US-11-241-596-204	Sequence 204, App	516	89.5	2.5	242	7	US-11-056-355B-4724	Sequence 4724, App
443	89.5	2.6	499	7	US-11-241-596-205	Sequence 205, App	517	89.5	2.5	272	6	US-10-953-349-32121	Sequence 32121, A
444	89.5	2.6	499	7	US-11-241-596-206	Sequence 206, App	518	89.5	2.5	287	7	US-11-056-355B-71099	Sequence 71099, A
445	89.5	2.6	499	7	US-11-241-596-207	Sequence 207, App	519	89.5	2.5	370	7	US-11-056-355B-71098	Sequence 71098, A
446	89.5	2.6	499	7	US-11-241-596-208	Sequence 208, App	520	89.5	2.5	376	7	US-11-330-403-19136	Sequence 19136, A
447	89.5	2.6	499	7	US-11-241-596-209	Sequence 209, App	521	89.5	2.5	386	7	US-11-056-355B-71097	Sequence 71097, A
448	89.5	2.6	499	7	US-11-241-596-210	Sequence 210, App	522	89.5	2.5	412	7	US-11-056-355B-12553	Sequence 12553, A
449	89.5	2.6	499	7	US-11-241-596-211	Sequence 211, App	523	89.5	2.5	414	7	US-11-056-355B-6572	Sequence 6572, App
450	89.5	2.6	499	7	US-11-241-596-212	Sequence 212, App	524	89.5	2.5	537	6	US-10-953-349-4553	Sequence 4553, App
451	89.5	2.6	499	7	US-11-241-596-213	Sequence 213, App	525	89.5	2.5	537	7	US-11-056-355B-28387	Sequence 28387, A
452	89.5	2.6	499	7	US-11-241-596-214	Sequence 214, App	526	89.5	2.5	537	7	US-11-056-355B-31977	Sequence 31977, A
453	89.5	2.6	499	7	US-11-241-596-215	Sequence 215, App	527	89.5	2.5	537	7	US-11-056-355B-84465	Sequence 84465, A
454	89.5	2.6	499	7	US-11-241-596-216	Sequence 216, App	528	89.5	2.5	546	7	US-11-330-403-10163	Sequence 10163, A
455	89.5	2.6	499	7	US-11-241-596-217	Sequence 217, App	529	89.5	2.5	559	7	US-11-316-521-45	Sequence 45, App1
456	89.5	2.6	499	7	US-11-241-596-218	Sequence 218, App	530	89.5	2.5	559	7	US-11-330-403-1505	Sequence 1505, App
457	89.5	2.6	499	7	US-11-241-596-219	Sequence 219, App	531	89.5	2.5	559	7	US-11-330-403-2392	Sequence 2392, App
458	89.5	2.6	499	7	US-11-241-596-220	Sequence 220, App	532	89.5	2.5	559	7	US-11-330-403-9433	Sequence 9433, App
459	89.5	2.6	499	7	US-11-241-596-221	Sequence 221, App	533	89.5	2.5	559	7	US-11-330-403-9654	Sequence 9654, App
460	89.5	2.6	499	7	US-11-241-596-222	Sequence 222, App	534	89.5	2.5	560	7	US-11-330-403-14413	Sequence 14413, A
461	89.5	2.6	499	7	US-11-241-596-223	Sequence 223, App	535	89.5	2.5	563	7	US-11-330-403-37293	Sequence 37293, App
462	89.5	2.6	499	7	US-11-241-596-224	Sequence 224, App	536	89.5	2.5	595	6	US-10-449-902-38085	Sequence 38085, App
463	89.5	2.6	499	7	US-11-241-596-225	Sequence 225, App	537	89.5	2.5	602	6	US-10-953-349-4552	Sequence 4552, App
464	89.5	2.6	499	7	US-11-241-596-226	Sequence 226, App	538	89.5	2.5	602	7	US-11-056-355B-28386	Sequence 28386, App
465	89.5	2.6	499	7	US-11-241-596-227	Sequence 227, App	539	89.5	2.5	602	7	US-11-056-355B-31976	Sequence 31976, A
466	89.5	2.6	499	7	US-11-241-596-228	Sequence 228, App	540	89.5	2.5	602	7	US-11-056-355B-84464	Sequence 84464, A
467	89.5	2.6	499	7	US-11-241-596-229	Sequence 229, App	541	89.5	2.5	634	7	US-11-330-403-323	Sequence 323, App

542	89	2.5	690	6	US-10-449-902-41507	Sequence 41507, A	615	87.5	2.5	469	7	US-11-330-403-16865	Sequence 16865, A
543	89	2.5	707	7	US-11-121-154-164	Sequence 164, App	616	87.5	2.5	534	7	US-11-056-355B-74171	Sequence 74171, A
544	89	2.5	767	7	US-11-121-154-63	Sequence 63, Appl	617	87.5	2.5	534	7	US-11-056-355B-79097	Sequence 79097, A
545	89	2.5	858	7	US-11-193-046-19	Sequence 19, Appl	618	87.5	2.5	534	7	US-11-056-355B-107996	Sequence 107996, A
546	89	2.5	869	7	US-11-193-046-17	Sequence 17, Appl	619	87.5	2.5	534	7	US-11-056-355B-119235	Sequence 119235, A
547	89	2.5	901	7	US-11-193-046-16	Sequence 16, Appl	620	87.5	2.5	534	7	US-11-330-403-2820	Sequence 2820, Ap
548	89	2.5	1186	7	US-11-121-154-57	Sequence 57, Appl	621	87.5	2.5	565	7	US-11-330-403-4171	Sequence 4171, Ap
549	89	2.5	1220	6	US-10-449-902-41253	Sequence 41253, A	622	87.5	2.5	573	7	US-11-056-355B-74170	Sequence 74170, A
550	89	2.5	10625	6	US-11-330-403-1837	Sequence 1837, Ap	623	87.5	2.5	576	7	US-11-056-355B-79096	Sequence 79096, A
551	88.5	2.5	211	6	US-10-449-902-40480	Sequence 40480, A	624	87.5	2.5	584	7	US-11-293-697-4839	Sequence 4839, Ap
552	88.5	2.5	271	7	US-11-056-355B-26294	Sequence 26294, A	625	87.5	2.5	678	7	US-11-056-355B-48015	Sequence 48015, A
553	88.5	2.5	355	6	US-10-449-902-54125	Sequence 54125, A	626	87.5	2.5	715	7	US-11-056-355B-74169	Sequence 74169, A
554	88.5	2.5	373	6	US-10-966-645-10	Sequence 10, Appl	627	87.5	2.5	760	7	US-11-056-355B-48014	Sequence 48014, A
555	88.5	2.5	377	6	US-10-953-349-17694	Sequence 17694, A	628	87.5	2.5	918	7	US-11-056-355B-48013	Sequence 48013, A
556	88.5	2.5	397	6	US-10-516-032-2	Sequence 2, Appl1	629	87.5	2.5	927	6	US-10-449-902-47854	Sequence 47854, A
557	88.5	2.5	429	7	US-11-056-355B-81955	Sequence 81955, A	630	87.5	2.5	955	6	US-10-449-902-41337	Sequence 41337, A
558	88.5	2.5	465	6	US-10-953-349-17693	Sequence 17693, A	631	87.5	2.5	955	6	US-10-471-571A-3910	Sequence 3910, Ap
559	88.5	2.5	478	7	US-11-330-403-1116	Sequence 1116, Ap	632	87.5	2.5	1087	6	US-10-406-020-15	Sequence 15, Appl
560	88.5	2.5	487	7	US-11-056-355B-83513	Sequence 83513, A	633	87.5	2.5	1369	6	US-10-449-902-42964	Sequence 42964, A
561	88.5	2.5	530	6	US-10-520-999-12	Sequence 12, Appl	634	87.5	2.5	1369	6	US-10-449-902-45778	Sequence 45778, A
562	88.5	2.5	530	6	US-11-204-186-4	Sequence 4, Appl1	635	87.5	2.5	4544	6	US-10-537-642-20	Sequence 20, Appl
563	88.5	2.5	532	7	US-11-330-403-18717	Sequence 18717, A	636	87	2.5	180	6	US-10-953-349-32357	Sequence 32357, A
564	88.5	2.5	557	7	US-11-293-697-2524	Sequence 2524, Ap	637	87	2.5	180	7	US-11-056-355B-64392	Sequence 64392, A
565	88.5	2.5	565	7	US-11-330-403-16604	Sequence 16604, A	638	87	2.5	185	6	US-10-953-349-39382	Sequence 39382, A
566	88.5	2.5	659	7	US-11-056-355B-81954	Sequence 81954, A	639	87	2.5	185	6	US-11-056-355B-1365	Sequence 1365, Ap
567	88.5	2.5	725	7	US-11-056-355B-81953	Sequence 81953, A	640	87	2.5	202	7	US-11-056-355B-64395	Sequence 64395, A
568	88.5	2.5	735	7	US-11-293-697-4881	Sequence 4881, Ap	641	87	2.5	339	7	US-11-056-355B-8949	Sequence 8950, Ap
569	88.5	2.5	853	6	US-10-449-902-55541	Sequence 55541, A	642	87	2.5	339	6	US-10-449-902-45596	Sequence 45596, A
570	88.5	2.5	864	6	US-10-449-902-41176	Sequence 41176, A	643	87	2.5	335	6	US-11-056-355B-8948	Sequence 8949, Ap
571	88.5	2.5	875	6	US-10-449-902-41316	Sequence 41316, A	644	87	2.5	335	7	US-11-056-355B-8948	Sequence 8949, Ap
572	88.5	2.5	906	6	US-10-449-902-41192	Sequence 41192, A	645	87	2.5	310	7	US-11-056-355B-25420	Sequence 25420, A
573	88.5	2.5	914	6	US-10-449-902-41306	Sequence 41306, A	646	87	2.5	339	6	US-10-449-902-31745	Sequence 31745, A
574	88.5	2.5	996	6	US-10-374-780A-512	Sequence 512, App	647	87	2.5	339	6	US-10-449-902-43299	Sequence 43299, A
575	88.5	2.5	1163	6	US-10-538-201-26	Sequence 26, Appl	648	87	2.5	339	6	US-10-449-902-55664	Sequence 55664, A
576	88.5	2.5	5178	6	US-10-700-439-178	Sequence 178, App	649	87	2.5	445	7	US-11-330-403-535A-22	Sequence 22, Appl
577	88.5	2.5	5179	7	US-11-105-233-185	Sequence 185, App	650	87	2.5	443	7	US-11-293-697-4448	Sequence 4448, Ap
578	88	2.5	248	6	US-10-449-902-53291	Sequence 53291, A	651	87	2.5	519	7	US-11-330-403-5895	Sequence 5895, Ap
579	88	2.5	329	7	US-11-286-216-2	Sequence 2, Appl1	652	87	2.5	559	7	US-11-330-403-4666	Sequence 4666, Ap
580	88	2.5	381	7	US-11-056-355B-42684	Sequence 42684, A	653	87	2.5	559	7	US-10-449-902-53097	Sequence 53097, A
581	88	2.5	381	7	US-11-056-355B-103851	Sequence 103851, A	654	87	2.5	558	7	US-11-296-092-69	Sequence 69, Appl
582	88	2.5	381	7	US-11-056-355B-115090	Sequence 115090, A	655	87	2.5	558	7	US-11-296-155-69	Sequence 69, Appl
583	88	2.5	416	6	US-10-953-349-32523	Sequence 32523, A	656	87	2.5	617	6	US-10-526-650-2	Sequence 2, Appl1
584	88	2.5	416	7	US-11-056-355B-67135	Sequence 67135, A	657	87	2.5	673	7	US-11-376-673-16	Sequence 16, Appl
585	88	2.5	442	7	US-11-289-989-6	Sequence 6, Appl1	658	87	2.5	678	6	US-11-101-316-1	Sequence 1, Appl
586	88	2.5	458	7	US-11-289-989-16	Sequence 16, Appl	659	87	2.5	680	6	US-10-517-420-52	Sequence 52, Appl
587	88	2.5	458	7	US-11-330-403-7010	Sequence 7010, Ap	660	87	2.5	680	6	US-10-449-902-47513	Sequence 47513, A
588	88	2.5	459	6	US-10-449-902-36720	Sequence 36720, A	661	87	2.5	687	6	US-10-449-902-41884	Sequence 41884, A
589	88	2.5	474	7	US-11-056-355B-8225	Sequence 8225, Ap	662	87	2.5	856	7	US-11-330-403-13531	Sequence 13531, A
590	88	2.5	477	7	US-11-056-355B-8224	Sequence 8224, Ap	663	87	2.5	856	7	US-10-538-201-5	Sequence 5, Appl1
591	88	2.5	483	7	US-11-056-355B-2713	Sequence 2713, Ap	664	87	2.5	1192	6	US-11-330-403-10696	Sequence 10696, A
592	88	2.5	563	7	US-11-330-403-14692	Sequence 14692, A	665	87	2.5	1367	7	US-10-505-928-357	Sequence 357, App
593	88	2.5	592	6	US-10-449-902-32680	Sequence 32680, A	666	87	2.5	167	6	US-10-953-349-37884	Sequence 37984, A
594	88	2.5	592	6	US-10-449-902-52392	Sequence 52392, A	667	86.5	2.5	172	6	US-10-953-349-37883	Sequence 37983, A
595	88	2.5	617	7	US-11-330-403-3068	Sequence 3068, Ap	668	86.5	2.5	285	6	US-11-056-355B-98826	Sequence 98826, A
596	88	2.5	634	6	US-10-449-902-44817	Sequence 44817, A	669	86.5	2.5	285	6	US-11-056-355B-98825	Sequence 98825, A
597	88	2.5	748	7	US-11-056-355B-71828	Sequence 71828, A	670	86.5	2.5	295	7	US-11-056-355B-110065	Sequence 110065, A
598	88	2.5	764	7	US-11-056-355B-71827	Sequence 71827, A	671	86.5	2.5	296	7	US-11-056-355B-110064	Sequence 110064, A
599	88	2.5	835	7	US-11-056-355B-71630	Sequence 71630, A	672	86.5	2.5	334	6	US-10-449-902-40000	Sequence 40000, A
600	88	2.5	835	7	US-11-056-355B-71629	Sequence 71629, A	673	86.5	2.5	335	6	US-10-449-902-45713	Sequence 45713, A
601	88	2.5	835	7	US-11-056-355B-71629	Sequence 71629, A	674	86.5	2.5	335	6	US-11-330-403-6974	Sequence 6974, Ap
602	88	2.5	855	6	US-10-449-902-33272	Sequence 33272, A	675	86.5	2.5	407	7	US-11-056-355B-62799	Sequence 62799, A
603	88	2.5	871	7	US-11-056-355B-71826	Sequence 71826, A	676	86.5	2.5	428	6	US-10-953-349-24425	Sequence 24425, A
604	88	2.5	1402	6	US-10-532-053-2	Sequence 2, Appl1	677	86.5	2.5	428	6	US-11-056-355B-59257	Sequence 59257, A
605	88	2.5	2478	6	US-10-471-571A-2278	Sequence 2278, Ap	678	86.5	2.5	432	7	US-11-056-355B-7077	Sequence 7077, Ap
606	87.5	2.5	182	7	US-11-056-355B-1134	Sequence 1134, Ap	679	86.5	2.5	434	6	US-10-534-419-10	Sequence 10, Appl
607	87.5	2.5	319	7	US-11-056-355B-42586	Sequence 42586, A	680	86.5	2.5	443	6	US-10-953-349-24424	Sequence 24424, A
608	87.5	2.5	319	7	US-11-056-355B-103853	Sequence 103853, A	681	86.5	2.5	443	6	US-11-056-355B-59256	Sequence 59256, A
609	87.5	2.5	319	7	US-11-056-355B-110592	Sequence 110592, A	682	86.5	2.5	443	7	US-11-330-403-19015	Sequence 19015, A
610	87.5	2.5	331	7	US-11-056-355B-42685	Sequence 42685, A	683	86.5	2.5	455	7	US-11-056-355B-12454	Sequence 12454, A
611	87.5	2.5	331	7	US-11-056-355B-103852	Sequence 103852, A	684	86.5	2.5	476	7	US-11-056-355B-48014	Sequence 48014, A
612	87.5	2.5	331	7	US-11-056-355B-115091	Sequence 115091, A	685	86.5	2.5	476	7	US-11-056-355B-12454	Sequence 12454, A
613	87.5	2.5	396	7	US-11-056-355B-96812	Sequence 96812, A	686	86.5	2.5	504	6	US-11-330-403-19211	Sequence 19211, A
614	87.5	2.5	416	7	US-11-293-697-4319	Sequence 4319, Ap	687	86.5	2.5	517	6	US-10-953-349-1089	Sequence 1089, Ap
							688	86.5	2.5	517	6	US-10-953-349-1089	Sequence 1089, Ap

689	86.5	2.5	518	6	US-10-449-902-48443	Sequence 48443, A	762	86	2.5	1523	7	US-11-056-355B-81254	Sequence 81254, A
690	86.5	2.5	523	6	US-10-449-902-45098	Sequence 45098, A	763	86	2.5	1832	7	US-11-330-403-11014	Sequence 11014, A
691	86.5	2.5	544	7	US-11-056-355B-87412	Sequence 87412, A	764	86	2.5	2732	6	US-10-506-666-43	Sequence 43, Appl
692	86.5	2.5	547	7	US-11-330-403-7900	Sequence 7900, Ap	765	85.5	2.4	138	7	US-11-174-307B-3336	Sequence 3336, Ap
693	86.5	2.5	568	7	US-11-056-355B-4036	Sequence 4036, Ap	766	85.5	2.4	175	7	US-11-056-355B-1135	Sequence 1135, Ap
694	86.5	2.5	568	7	US-11-056-355B-12453	Sequence 12453, A	767	85.5	2.4	196	7	US-11-056-355B-6356	Sequence 6356, A
695	86.5	2.5	578	6	US-10-953-349-5109	Sequence 5109, Ap	768	85.5	2.4	289	7	US-11-056-355B-65092	Sequence 65092, A
696	86.5	2.5	578	7	US-11-056-355B-41621	Sequence 41621, A	769	85.5	2.4	338	6	US-10-449-902-55375	Sequence 55375, A
697	86.5	2.5	578	7	US-11-056-355B-106425	Sequence 106425, A	770	85.5	2.4	334	6	US-10-953-349-37039	Sequence 37039, A
698	86.5	2.5	578	7	US-11-056-355B-117664	Sequence 117664, A	771	85.5	2.4	364	6	US-10-953-349-35603	Sequence 35603, A
699	86.5	2.5	587	7	US-11-056-355B-87411	Sequence 87411, A	772	85.5	2.4	367	6	US-10-953-349-37038	Sequence 37038, A
700	86.5	2.5	587	7	US-11-056-355B-87410	Sequence 87410, A	773	85.5	2.4	359	7	US-11-056-355B-75524	Sequence 75524, A
701	86.5	2.5	598	6	US-10-953-349-5108	Sequence 5108, Ap	774	85.5	2.4	425	6	US-10-449-902-56607	Sequence 56607, A
702	86.5	2.5	598	7	US-11-056-355B-2139	Sequence 2139, Ap	775	85.5	2.4	442	6	US-10-953-349-32269	Sequence 32269, A
703	86.5	2.5	598	7	US-11-056-355B-15443	Sequence 15443, A	776	85.5	2.4	453	7	US-11-056-355B-75523	Sequence 75523, A
704	86.5	2.5	598	7	US-11-056-355B-41621	Sequence 41621, A	777	85.5	2.4	462	6	US-10-953-349-32765	Sequence 32765, A
705	86.5	2.5	598	7	US-11-056-355B-106424	Sequence 106424, A	778	85.5	2.4	462	7	US-11-056-355B-67037	Sequence 67037, A
706	86.5	2.5	598	7	US-11-056-355B-117663	Sequence 117663, A	779	85.5	2.4	481	7	US-11-056-355B-50415	Sequence 50415, A
707	86.5	2.5	600	6	US-10-953-349-5107	Sequence 5107, Ap	780	85.5	2.4	486	7	US-11-056-355B-50414	Sequence 50414, A
708	86.5	2.5	600	7	US-11-056-355B-41619	Sequence 41619, A	781	85.5	2.4	487	7	US-11-056-355B-75522	Sequence 75522, A
709	86.5	2.5	600	7	US-11-056-355B-117662	Sequence 117662, A	782	85.5	2.4	497	7	US-11-056-355B-95413	Sequence 95413, A
710	86.5	2.5	600	7	US-11-056-355B-81223	Sequence 81223, A	783	85.5	2.4	508	6	US-10-953-349-32268	Sequence 32268, A
711	86.5	2.5	637	7	US-11-056-355B-81222	Sequence 81222, A	784	85.5	2.4	521	6	US-10-953-349-32267	Sequence 32267, A
712	86.5	2.5	647	7	US-11-056-355B-81221	Sequence 81221, A	785	85.5	2.4	628	7	US-11-358-419-48	Sequence 48, Appl
713	86.5	2.5	657	7	US-11-056-355B-81221	Sequence 81221, A	786	85.5	2.4	821	6	US-10-449-902-41595	Sequence 41595, A
714	86.5	2.5	661	6	US-10-449-902-37700	Sequence 37700, A	787	85.5	2.4	943	6	US-10-540-89B-106	Sequence 106, App
715	86.5	2.5	706	6	US-10-449-902-37700	Sequence 37700, A	788	85.5	2.4	944	6	US-10-449-902-47242	Sequence 47242, A
716	86.5	2.5	858	6	US-10-449-902-41120	Sequence 41120, A	789	85.5	2.4	990	6	US-10-540-89B-108	Sequence 108, App
717	86.5	2.5	895	6	US-10-449-902-41120	Sequence 41120, A	790	85.5	2.4	1066	6	US-10-370-959-2	Sequence 2, Appl
718	86.5	2.5	908	7	US-11-134-228A-67	Sequence 67, Appl	791	85.5	2.4	1066	7	US-11-302-678-50	Sequence 50, Appl
719	86.5	2.5	1048	6	US-10-520-783-82	Sequence 22, Appl	792	85.5	2.4	1189	6	US-10-449-902-41123	Sequence 41123, A
720	86.5	2.5	1090	6	US-10-530-450-10	Sequence 10, Appl	793	85	2.4	201	6	US-10-953-349-29774	Sequence 29274, A
721	86.5	2.5	1252	6	US-10-449-902-55024	Sequence 55024, A	794	85	2.4	255	6	US-10-449-902-56595	Sequence 56595, A
722	86.5	2.5	1478	7	US-11-330-403-5386	Sequence 5386, Ap	795	85	2.4	256	7	US-11-056-355B-67385	Sequence 67385, A
723	86.5	2.5	2026	6	US-10-505-928-831	Sequence 831, Ap	796	85	2.4	261	7	US-11-056-355B-7112	Sequence 7112, Ap
724	86.5	2.5	2804	7	US-11-330-403-12380	Sequence 12380, A	797	85	2.4	269	6	US-10-953-349-31119	Sequence 31119, A
725	86	2.5	177	6	US-10-953-349-32339	Sequence 32339, A	798	85	2.4	307	6	US-10-953-349-28520	Sequence 28520, A
726	86	2.5	177	7	US-11-056-355B-63146	Sequence 63146, A	799	85	2.4	307	7	US-11-056-355B-65408	Sequence 65408, A
727	86	2.5	279	7	US-11-293-697-4737	Sequence 4737, Ap	800	85	2.4	350	7	US-11-330-403-14463	Sequence 14463, A
728	86	2.5	319	7	US-11-056-355B-11958	Sequence 11958, A	801	85	2.4	397	6	US-10-471-571K-2216	Sequence 2216, Ap
729	86	2.5	319	7	US-11-056-355B-20183	Sequence 20183, A	802	85	2.4	403	7	US-11-056-355B-6620	Sequence 6620, Ap
730	86	2.5	336	6	US-10-953-349-4594	Sequence 4594, Ap	803	85	2.4	441	7	US-11-056-355B-72978	Sequence 72978, A
731	86	2.5	336	7	US-11-056-355B-28388	Sequence 28388, A	804	85	2.4	449	7	US-11-330-403-10435	Sequence 10435, A
732	86	2.5	336	7	US-11-056-355B-31978	Sequence 31978, A	805	85	2.4	560	7	US-11-330-403-11913	Sequence 11913, A
733	86	2.5	336	7	US-11-056-355B-77804	Sequence 77804, A	806	85	2.4	566	7	US-11-330-403-3255	Sequence 3255, Ap
734	86	2.5	336	7	US-11-056-355B-84466	Sequence 84466, A	807	85	2.4	614	6	US-10-449-902-51430	Sequence 51430, A
735	86	2.5	358	7	US-11-330-403-1055	Sequence 1055, Ap	808	85	2.4	641	6	US-10-449-902-47052	Sequence 47052, A
736	86	2.5	363	7	US-11-056-355B-62800	Sequence 62800, A	809	85	2.4	646	7	US-10-449-902-412018	Sequence 12018, A
737	86	2.5	363	6	US-10-449-902-45768	Sequence 45768, A	810	85	2.4	709	6	US-10-449-902-41887	Sequence 41887, A
738	86	2.5	419	7	US-11-330-403-9081	Sequence 9081, Ap	811	85	2.4	735	6	US-10-529-931-10	Sequence 10, Appl
739	86	2.5	437	7	US-11-056-355B-8297	Sequence 8297, Ap	812	85	2.4	746	6	US-10-449-902-41555	Sequence 41555, A
740	86	2.5	444	7	US-11-056-355B-8296	Sequence 8296, Ap	813	85	2.4	808	6	US-10-449-902-44460	Sequence 44460, A
741	86	2.5	462	7	US-11-056-355B-8295	Sequence 8295, Ap	814	85	2.4	901	6	US-10-531-659-17	Sequence 17, Appl
742	86	2.5	508	6	US-10-449-902-30106	Sequence 30106, A	815	85	2.4	946	6	US-10-449-902-42263	Sequence 42263, A
743	86	2.5	546	7	US-11-330-403-6933	Sequence 6933, Ap	816	85	2.4	947	6	US-10-449-902-41264	Sequence 41264, A
744	86	2.5	546	7	US-11-330-403-17434	Sequence 17434, A	817	85	2.4	963	6	US-10-142-2758-4	Sequence 4, Appl1
745	86	2.5	608	7	US-11-056-355B-45804	Sequence 45804, A	818	85	2.4	1008	7	US-11-288-992-11	Sequence 11, Appl
746	86	2.5	608	7	US-11-056-355B-73306	Sequence 73306, A	819	85	2.4	1037	6	US-10-449-902-43335	Sequence 43335, A
747	86	2.5	608	7	US-11-056-355B-77695	Sequence 77695, A	820	85	2.4	1054	7	US-11-288-992-47	Sequence 47, Appl
748	86	2.5	667	7	US-11-056-355B-45803	Sequence 45803, A	821	85	2.4	1122	7	US-11-330-403-16472	Sequence 16472, A
749	86	2.5	667	7	US-11-056-355B-77884	Sequence 77884, A	822	85	2.4	1227	6	US-10-449-902-41274	Sequence 41274, A
750	86	2.5	695	6	US-10-533-054-16	Sequence 16, Appl	823	85	2.4	1246	6	US-10-540-89B-409	Sequence 409, Appl
751	86	2.5	743	6	US-10-449-902-37717	Sequence 37717, A	824	85	2.4	1384	6	US-10-529-931-18	Sequence 18, Appl
752	86	2.5	760	6	US-10-539-228-614	Sequence 614, App	825	85	2.4	1394	6	US-10-529-931-22	Sequence 22, Appl
753	86	2.5	881	6	US-10-539-228-174	Sequence 374, App	826	85	2.4	2517	7	US-11-883-329-204	Sequence 204, App
754	86	2.5	914	7	US-11-330-403-8991	Sequence 8991, Ap	827	84.5	2.4	136	6	US-10-449-902-33631	Sequence 33631, A
755	86	2.5	945	6	US-10-449-902-41367	Sequence 41367, A	828	84.5	2.4	221	7	US-11-056-355B-98827	Sequence 98827, A
756	86	2.5	1053	6	US-10-449-902-41514	Sequence 41514, A	829	84.5	2.4	221	7	US-11-056-355B-110066	Sequence 110066, A
757	86	2.5	1071	6	US-10-539-228-857	Sequence 857, App	830	84.5	2.4	226	6	US-10-953-349-28687	Sequence 28687, A
758	86	2.5	1244	7	US-11-299-791-16	Sequence 16, Appl	831	84.5	2.4	236	7	US-11-056-355B-68288	Sequence 68288, A
759	86	2.5	1455	7	US-11-314-018-30	Sequence 20, Appl	832	84.5	2.4	251	6	US-10-953-349-28686	Sequence 28686, A
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761	86	2.5	1510	7	US-11-056-355B-81255	Sequence 81255, A	834	84.5	2.4	251	7	US-11-056-355B-66287	Sequence 66287, A

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836	84.5	2.4	284	7	US-11-056-355B-10331	Sequence 10331, A	909	84	2.4	705	6	US-10-449-902-37508	Sequence 37508, A
837	84.5	2.4	278	7	US-11-330-403-9112	Sequence 9112, Ap	910	84	2.4	718	6	US-10-449-902-33412	Sequence 43412, A
838	84.5	2.4	286	7	US-11-056-355B-10320	Sequence 10320, A	911	84	2.4	732	6	US-10-449-902-6957	Sequence 46957, A
839	84.5	2.4	296	6	US-10-953-349-28685	Sequence 28685, A	912	84	2.4	732	6	US-10-756-047-2	Sequence 2, Appl1
840	84.5	2.4	296	7	US-11-056-355B-68286	Sequence 68286, A	913	84	2.4	734	6	US-10-953-349-10604	Sequence 10604, A
841	84.5	2.4	315	7	US-11-056-355B-10319	Sequence 10319, A	914	84	2.4	738	6	US-10-953-349-10603	Sequence 10603, A
842	84.5	2.4	319	6	US-10-953-349-36568	Sequence 36568, A	915	84	2.4	742	6	US-11-284-236-63	Sequence 63, Appl1
843	84.5	2.4	404	7	US-11-056-355B-107641	Sequence 107641, A	916	84	2.4	772	6	US-10-449-902-11332	Sequence 41362, A
844	84.5	2.4	404	7	US-11-056-355B-118880	Sequence 118880, A	917	84	2.4	777	6	US-10-553-520-103	Sequence 103, App
845	84.5	2.4	412	7	US-11-056-355B-2285	Sequence 2285, Ap	918	84	2.4	915	6	US-10-449-902-43511	Sequence 43511, A
846	84.5	2.4	412	7	US-11-056-355B-12398	Sequence 12398, A	919	84	2.4	925	6	US-10-449-902-41466	Sequence 41466, A
847	84.5	2.4	451	7	US-11-330-403-8644	Sequence 8644, Ap	920	84	2.4	925	6	US-11-293-697-3889	Sequence 3889, Ap
848	84.5	2.4	485	6	US-10-953-349-36036	Sequence 36036, A	921	84	2.4	964	6	US-10-142-275B-2	Sequence 2, Appl1
849	84.5	2.4	485	7	US-11-056-355B-10253	Sequence 10253, A	922	84	2.4	1070	6	US-10-449-902-11489	Sequence 41489, A
850	84.5	2.4	505	6	US-11-330-403-13762	Sequence 13762, A	923	84	2.4	1401	7	US-11-056-355B-70799	Sequence 70799, A
851	84.5	2.4	521	6	US-10-953-349-35631	Sequence 35631, A	924	84	2.4	1500	6	US-10-540-698-85	Sequence 85, Appl1
852	84.5	2.4	522	7	US-11-293-697-4162	Sequence 4162, Ap	925	84	2.4	2359	6	US-10-374-780A-1066	Sequence 1066, Ap
853	84.5	2.4	532	7	US-11-330-403-16523	Sequence 16523, A	926	84	2.4	4590	6	US-10-505-928-569	Sequence 569, App
854	84.5	2.4	543	7	US-11-301-554-337	Sequence 337, App	927	83.5	2.4	138	6	US-10-953-349-39866	Sequence 39866, A
855	84.5	2.4	543	7	US-11-317-330A-21	Sequence 21, Appl1	928	83.5	2.4	202	6	US-10-953-349-51344	Sequence 21344, A
856	84.5	2.4	552	6	US-10-953-349-35630	Sequence 35630, A	929	83.5	2.4	202	7	US-11-056-355B-56485	Sequence 56485, A
857	84.5	2.4	605	7	US-11-056-355B-67285	Sequence 67285, A	930	83.5	2.4	212	6	US-10-953-349-769	Sequence 769, App
858	84.5	2.4	606	6	US-10-449-902-48918	Sequence 48918, A	931	83.5	2.4	212	7	US-11-056-355B-25892	Sequence 25892, A
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863	84.5	2.4	793	7	US-11-330-403-13739	Sequence 13739, A	936	83.5	2.4	216	7	US-11-056-355B-106349	Sequence 106349, A
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865	84.5	2.4	871	6	US-10-449-902-11121	Sequence 41121, A	938	83.5	2.4	217	6	US-10-953-349-18120	Sequence 18120, A
866	84.5	2.4	914	6	US-10-449-902-51797	Sequence 51797, A	939	83.5	2.4	217	7	US-11-056-355B-67960	Sequence 67960, A
867	84.5	2.4	960	7	US-11-256-173-15	Sequence 15, Appl1	940	83.5	2.4	247	6	US-10-953-349-11819	Sequence 11819, A
868	84.5	2.4	1057	7	US-11-293-697-3230	Sequence 3230, Ap	941	83.5	2.4	379	1	US-09-949-925-138	Sequence 138, App
869	84.5	2.4	1069	7	US-11-375-615-50	Sequence 50, Appl1	942	83.5	2.4	414	7	US-11-056-355B-8324	Sequence 8324, Ap
870	84.5	2.4	1142	7	US-11-192-644-11	Sequence 11, Appl1	943	83.5	2.4	415	6	US-10-953-349-11523	Sequence 11523, A
871	84.5	2.4	1263	6	US-10-540-898-339	Sequence 539, App	944	83.5	2.4	328	7	US-11-056-355B-53363	Sequence 53363, A
872	84.5	2.4	1504	6	US-10-374-780A-1457	Sequence 1457, Ap	945	83.5	2.4	334	6	US-10-953-349-33563	Sequence 33563, A
873	84.5	2.4	1743	7	US-11-248-956-32	Sequence 32, Appl1	946	83.5	2.4	360	7	US-11-056-355B-57686	Sequence 57686, A
874	84.5	2.4	2304	6	US-10-540-898-310	Sequence 310, A	947	83.5	2.4	425	6	US-10-953-349-573561	Sequence 573561, A
875	84.5	2.4	2314	7	US-11-013-711-11	Sequence 11, Appl1	948	83.5	2.4	427	7	US-11-056-355B-53362	Sequence 53362, A
876	84.5	2.4	3696	7	US-11-330-363-4	Sequence 4, Appl1	949	83.5	2.4	427	7	US-11-056-355B-8324	Sequence 8324, Ap
877	84	2.4	131	7	US-11-056-355B-65960	Sequence 65960, A	950	83.5	2.4	417	6	US-10-953-349-83562	Sequence 83562, A
878	84	2.4	239	6	US-10-953-349-12628	Sequence 12628, A	951	83.5	2.4	417	6	US-11-056-355B-57685	Sequence 57685, A
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882	84	2.4	275	6	US-11-317-789A-512	Sequence 512, App	955	83.5	2.4	431	6	US-10-449-902-55232	Sequence 55232, A
883	84	2.4	282	6	US-10-449-902-40106	Sequence 40106, A	956	83.5	2.4	450	6	US-10-953-349-9835	Sequence 9835, Ap
884	84	2.4	337	6	US-10-953-349-39161	Sequence 39161, A	957	83.5	2.4	457	7	US-11-330-403-1428	Sequence 1428, Ap
885	84	2.4	351	6	US-10-953-349-39160	Sequence 39160, A	958	83.5	2.4	461	6	US-10-953-349-11532	Sequence 11532, A
886	84	2.4	365	7	US-11-056-355B-81599	Sequence 81599, A	959	83.5	2.4	464	7	US-11-330-403-8525	Sequence 8525, Ap
887	84	2.4	366	6	US-10-953-349-39159	Sequence 39159, A	960	83.5	2.4	467	7	US-11-056-355B-11827	Sequence 11827, A
888	84	2.4	402	7	US-11-056-355B-81598	Sequence 81598, A	961	83.5	2.4	472	7	US-11-056-355B-12250	Sequence 12250, A
889	84	2.4	409	7	US-11-056-355B-7707	Sequence 7707, Ap	962	83.5	2.4	498	6	US-10-471-571A-5268	Sequence 5268, Ap
890	84	2.4	420	6	US-10-449-902-7050	Sequence 7050, A	963	83.5	2.4	503	6	US-11-330-403-9033	Sequence 9033, Ap
891	84	2.4	420	6	US-10-449-902-48480	Sequence 48480, A	964	83.5	2.4	515	7	US-11-293-697-3041	Sequence 3041, Ap
892	84	2.4	420	6	US-11-056-355B-7706	Sequence 7706, Ap	965	83.5	2.4	535	6	US-10-449-902-45304	Sequence 45304, A
893	84	2.4	434	7	US-11-056-355B-7705	Sequence 7705, Ap	966	83.5	2.4	535	7	US-11-330-403-6400	Sequence 6400, Ap
894	84	2.4	460	7	US-11-330-403-7956	Sequence 7956, Ap	967	83.5	2.4	547	6	US-10-449-902-38754	Sequence 38754, A
895	84	2.4	473	7	US-11-242-505A-42	Sequence 42, Appl1	968	83.5	2.4	556	7	US-11-330-403-6234	Sequence 6234, Ap
896	84	2.4	485	7	US-11-174-307B-3070	Sequence 3070, Ap	969	83.5	2.4	559	6	US-10-449-902-31532	Sequence 31532, A
897	84	2.4	492	6	US-10-953-349-29544	Sequence 29544, A	970	83.5	2.4	559	6	US-10-449-902-42917	Sequence 42917, A
898	84	2.4	492	7	US-11-056-355B-65652	Sequence 65652, A	971	83.5	2.4	561	7	US-11-330-403-11895	Sequence 11895, A
899	84	2.4	497	7	US-11-330-403-15601	Sequence 15601, A	972	83.5	2.4	590	7	US-11-330-403-18631	Sequence 18631, A
900	84	2.4	557	7	US-11-330-403-7181	Sequence 7181, Ap	973	83.5	2.4	620	7	US-11-293-697-3458	Sequence 3458, Ap
901	84	2.4	559	7	US-11-330-403-13449	Sequence 13449, A	974	83.5	2.4	638	7	US-11-330-403-15603	Sequence 15603, A
902	84	2.4	559	7	US-11-330-403-13449	Sequence 13449, A	975	83.5	2.4	694	6	US-10-505-928-312	Sequence 312, App
903	84	2.4	563	6	US-10-953-349-44341	Sequence 34341, A	976	83.5	2.4	758	6	US-10-449-902-44794	Sequence 44794, A
904	84	2.4	564	6	US-10-511-937-2557	Sequence 2557, Ap	977	83.5	2.4	733	7	US-11-056-355B-81262	Sequence 81262, A
905	84	2.4	565	6	US-10-953-349-43430	Sequence 34340, A	978	83.5	2.4	847	6	US-10-449-902-39944	Sequence 39944, A
906	84	2.4	566	6	US-10-449-902-49830	Sequence 49830, A	979	83.5	2.4	863	7	US-11-289-102-215	Sequence 215, App
907	84	2.4	602	6	US-10-449-902-41945	Sequence 41945, A	980	83.5	2.4	863	7	US-11-289-102-264	Sequence 264, App

981	83.5	2.4	894	6	US-10-449-902-52757	Sequence 52757, A	1054	82.5	2.4	352	7	US-11-330-403-2226	Sequence 2226, Ap
982	83.5	2.4	931	6	US-10-449-902-41196	Sequence 41196, A	1055	82.5	2.4	359	7	US-11-056-3558-13429	Sequence 13429, A
983	83.5	2.4	949	7	US-11-330-403-11692	Sequence 11692, A	1056	82.5	2.4	377	7	US-11-330-403-13616	Sequence 13616, A
984	83.5	2.4	982	6	US-10-449-902-41115	Sequence 41115, A	1057	82.5	2.4	411	7	US-11-296-092-83	Sequence 83, Appl
985	83.5	2.4	1128	6	US-10-449-902-52156	Sequence 52156, A	1058	82.5	2.4	431	7	US-11-296-155-83	Sequence 83, Appl
986	83.5	2.4	1230	6	US-10-539-723-2	Sequence 2, Appl1	1059	82.5	2.4	442	7	US-11-330-403-12347	Sequence 12347, A
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988	83.5	2.4	1356	6	US-10-480-962-16	Sequence 16, Appl	1061	82.5	2.4	470	6	US-10-449-902-43119	Sequence 43119, A
989	83.5	2.4	1531	6	US-10-540-898-142	Sequence 142, App	1062	82.5	2.4	471	7	US-11-056-3558-93150	Sequence 93150, Ap
990	83	2.4	169	6	US-10-953-349-3743	Sequence 3743, A	1063	82.5	2.4	475	6	US-10-449-902-48059	Sequence 48059, A
991	83	2.4	169	7	US-11-056-3558-101869	Sequence 116859, A	1064	82.5	2.4	475	6	US-11-056-3558-66385	Sequence 66385, A
992	83	2.4	171	7	US-11-056-3558-101869	Sequence 113108, A	1065	82.5	2.4	475	7	US-11-330-403-16518	Sequence 16518, A
993	83	2.4	171	7	US-11-056-3558-113108	Sequence 113108, A	1066	82.5	2.4	475	7	US-11-330-403-8012	Sequence 8012, App
994	83	2.4	173	7	US-11-056-3558-101868	Sequence 113107, A	1067	82.5	2.4	486	7	US-11-330-403-322	Sequence 322, App
995	83	2.4	173	7	US-11-056-3558-113107	Sequence 113107, A	1068	82.5	2.4	500	7	US-11-330-403-322	Sequence 322, App
996	83	2.4	192	6	US-10-953-349-34478	Sequence 34478, A	1069	82.5	2.4	523	7	US-11-056-3558-37515	Sequence 37515, A
997	83	2.4	227	6	US-10-449-902-52976	Sequence 52976, A	1070	82.5	2.4	534	7	US-11-056-3558-37514	Sequence 37514, A
998	83	2.4	235	6	US-10-953-349-37328	Sequence 37328, A	1071	82.5	2.4	548	7	US-11-056-3558-80831	Sequence 80831, A
999	83	2.4	238	6	US-11-056-3558-16850	Sequence 16850, A	1072	82.5	2.4	556	7	US-11-330-403-8284	Sequence 8284, Ap
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1001	83	2.4	318	7	US-11-056-3558-52921	Sequence 52921, A	1074	82.5	2.4	587	7	US-11-316-5355-173	Sequence 173, App
1002	83	2.4	323	6	US-10-953-349-33742	Sequence 33742, A	1075	82.5	2.4	613	6	US-10-953-349-32709	Sequence 32709, A
1003	83	2.4	332	7	US-11-056-3558-11648	Sequence 11648, A	1076	82.5	2.4	613	7	US-11-056-3558-66861	Sequence 66861, A
1004	83	2.4	341	6	US-10-953-349-35604	Sequence 35604, A	1077	82.5	2.4	624	7	US-11-056-3558-66475	Sequence 66475, A
1005	83	2.4	352	7	US-11-056-3558-52920	Sequence 52920, A	1078	82.5	2.4	636	7	US-11-293-697-247	Sequence 2497, Ap
1006	83	2.4	366	6	US-10-449-902-56415	Sequence 56415, A	1079	82.5	2.4	761	6	US-10-449-902-44017	Sequence 44017, Ap
1007	83	2.4	371	6	US-10-953-349-26639	Sequence 26639, A	1080	82.5	2.4	792	6	US-10-471-5718-4714	Sequence 4714, Ap
1008	83	2.4	371	6	US-11-056-3558-69266	Sequence 69266, A	1081	82.5	2.4	823	7	US-11-192-046-14	Sequence 14, Appl
1009	83	2.4	393	6	US-10-516-032-6	Sequence 6, Appl1	1082	82.5	2.4	840	6	US-10-449-902-41113	Sequence 41113, A
1010	83	2.4	396	7	US-11-330-403-484	Sequence 2484, Ap	1083	82.5	2.4	851	7	US-11-192-046-13	Sequence 13, Appl
1011	83	2.4	424	7	US-11-056-3558-68614	Sequence 68614, A	1084	82.5	2.4	862	7	US-11-192-046-12	Sequence 12, Appl
1012	83	2.4	436	6	US-10-953-349-34012	Sequence 34012, A	1085	82.5	2.4	880	7	US-11-192-046-11	Sequence 11, Appl
1013	83	2.4	448	7	US-11-293-697-4755	Sequence 4755, Ap	1086	82.5	2.4	914	6	US-10-700-439-180	Sequence 180, App
1014	83	2.4	452	7	US-11-251-465-26	Sequence 26, Appl	1087	82.5	2.4	1043	7	US-11-293-697-3024	Sequence 3024, Ap
1015	83	2.4	460	7	US-11-330-403-12416	Sequence 12416, A	1088	82.5	2.4	1086	7	US-11-330-403-3535	Sequence 3535, Ap
1016	83	2.4	469	6	US-10-449-902-50528	Sequence 50528, A	1089	82.5	2.4	1614	6	US-10-505-928-199	Sequence 199, App
1017	83	2.4	475	7	US-11-056-3558-68613	Sequence 68613, A	1090	82	2.3	169	7	US-11-056-3558-9128	Sequence 9128, Ap
1018	83	2.4	490	6	US-10-953-349-10390	Sequence 10390, A	1091	82	2.3	220	6	US-10-449-902-45122	Sequence 45122, A
1019	83	2.4	498	6	US-10-953-349-32642	Sequence 32642, A	1092	82	2.3	256	6	US-10-449-902-37045	Sequence 37045, A
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1021	83	2.4	500	7	US-11-330-403-11838	Sequence 11838, A	1094	82	2.3	286	7	US-11-056-3558-57878	Sequence 57878, A
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1023	83	2.4	531	7	US-10-953-349-1758	Sequence 7159, Ap	1096	82	2.3	306	7	US-11-056-3558-57876	Sequence 57876, A
1024	83	2.4	531	7	US-11-056-3558-28835	Sequence 28835, A	1097	82	2.3	310	6	US-10-449-902-33348	Sequence 33348, A
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1035	83	2.4	671	6	US-10-953-349-34214	Sequence 34214, A	1108	82	2.3	438	7	US-11-204-295-9	Sequence 9, Appl1
1036	83	2.4	677	7	US-11-330-403-7733	Sequence 7733, Ap	1109	82	2.3	438	7	US-11-203-820-9	Sequence 9, Appl1
1037	83	2.4	740	6	US-10-449-902-48395	Sequence 48395, A	1110	82	2.3	442	7	US-11-330-403-7420	Sequence 7420, Ap
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1042	83	2.4	1122	7	US-11-330-403-5867	Sequence 5867, Ap	1115	82	2.3	507	6	US-10-449-902-54321	Sequence 54321, A
1043	83	2.4	1263	6	US-10-471-5718-5118	Sequence 5118, Ap	1116	82	2.3	518	7	US-11-330-403-16143	Sequence 16143, A
1044	83	2.4	1263	6	US-10-539-228-723	Sequence 723, App	1117	82	2.3	546	6	US-11-330-403-70245	Sequence 70245, Ap
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1139	82	2.3	932	7	US-11-056-355B-92399	Sequence 92399, A	1212	81.5	2.3	1464	7	US-11-283-329-1552	Sequence 152, App
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1141	82	2.3	961	7	US-11-056-355B-92398	Sequence 92398, A	1214	81.5	2.3	1944	7	US-11-330-363-3	Sequence 3, App1
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1145	82	2.3	1160	6	US-11-192-046-650	Sequence 250, App	1218	81.5	2.3	285	7	US-11-330-403-938	Sequence 938, App
1146	82	2.3	1255	7	US-11-105-233-184	Sequence 184, App	1219	81.5	2.3	289	7	US-11-056-355B-6287	Sequence 2287, App
1147	82	2.3	1255	7	US-11-043-842-805	Sequence 805, App	1220	81.5	2.3	300	7	US-11-056-355B-63976	Sequence 63976, A
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1163	81.5	2.3	308	6	US-10-449-902-56383	Sequence 56383, A	1236	81.5	2.3	401	7	US-11-330-403-5587	Sequence 5587, App
1164	81.5	2.3	312	6	US-10-953-349-21493	Sequence 31493, A	1237	81.5	2.3	405	7	US-11-056-355B-5811	Sequence 5811, App
1165	81.5	2.3	312	6	US-11-056-355B-68325	Sequence 68325, A	1238	81.5	2.3	415	6	US-10-953-349-27098	Sequence 27098, A
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1176	81.5	2.3	444	7	US-11-330-403-5265	Sequence 5265, App	1249	81.5	2.3	466	7	US-11-056-355B-6130	Sequence 6130, App
1177	81.5	2.3	464	6	US-10-953-349-32643	Sequence 32643, A	1250	81.5	2.3	506	7	US-11-056-355B-6129	Sequence 6129, App
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1185	81.5	2.3	477	6	US-10-953-349-2612	Sequence 2612, App	1258	81.5	2.3	603	7	US-11-330-403-4201	Sequence 4201, App
1186	81.5	2.3	477	6	US-10-568-741-60	Sequence 40931, App1	1259	81.5	2.3	610	6	US-10-953-349-39539	Sequence 39539, A
1187	81.5	2.3	477	7	US-11-056-355B-40931	Sequence 40931, A	1260	81.5	2.3	632	7	US-11-245-628-37	Sequence 37, App1
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1192	81.5	2.3	559	7	US-11-330-403-1361	Sequence 1361, App	1265	81.5	2.3	663	7	US-11-056-355B-99583	Sequence 99583, A
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1198	81.5	2.3	638	7	US-11-330-403-1565	Sequence 1565, App	1271	81.5	2.3	806	6	US-10-953-349-8640	Sequence 8640, App
1199	81.5	2.3	655	7	US-11-293-697-3396	Sequence 3396, App	1272	81.5	2.3	806	7	US-11-056-355B-21132	Sequence 21132, A
													Sequence 99582, A

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1275	81	2.3	815	6	US-10-953-349-8639	Sequence 8639, Ap	1348	80.5	2.3	856	6	US-10-953-349-9319	Sequence 9339, Ap
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19	1129.5	32.3	550	2	US-09-949-016-6452
20	1129.5	32.3	550	2	US-09-909-064-227
21	1129.5	32.3	550	2	US-09-905-381A-227
22	1129.5	32.3	550	2	US-09-906-618-227
23	1129.5	32.3	550	2	US-09-906-646-227
24	1129.5	32.3	550	2	US-09-904-462-227
25	1129.5	32.3	550	2	US-09-902-736A-227
26	1129.5	32.3	550	2	US-09-906-722A-227

27	1129.5	32.3	550	2	US-09-905-449-227	Sequence 227, App
28	1129.5	32.3	550	2	US-09-903-562B-227	Sequence 227, App
29	1129.5	32.3	550	2	US-09-906-679A-227	Sequence 227, App
30	1129.5	32.3	550	3	US-09-394-264-2	Sequence 2, Appli
31	1129.5	32.3	550	3	US-09-907-841-227	Sequence 227, App
32	1129.5	32.3	550	3	US-09-949-016-8845	Sequence 8845, App
33	1129.5	32.3	550	2	US-09-949-016-8294	Sequence 8294, App
34	1121.5	32.0	575	2	US-09-579-288-5	Sequence 5, Appli
35	1113	31.8	552	3	US-09-394-264-7	Sequence 37, Appli
36	501.5	14.3	496	1	US-08-462-128-17	Sequence 37, Appli
37	501.5	14.3	496	1	US-08-463-180-37	Sequence 37, Appli
38	501.5	14.3	496	1	US-08-001-078A-1	Sequence 1, Appli
39	501.5	14.3	496	1	US-08-897-443-4	Sequence 4, Appli
40	501.5	14.3	496	1	US-08-463-218-1	Sequence 1, Appli
41	501.5	14.3	496	1	US-09-949-016-11306	Sequence 11306, A
42	501.5	14.3	496	5	PCT-US94-00253-1	Sequence 1, Appli
43	434	12.4	584	2	US-09-949-016-10340	Sequence 10340, A
44	434	12.4	584	2	US-09-949-016-10341	Sequence 10341, A
45	412	11.8	1036	2	US-10-104-047-2812	Sequence 2812, Ap
46	388.5	11.1	149	3	US-09-394-264-5	Sequence 5, Appli
47	370	10.6	915	2	US-09-907-794A-34	Sequence 34, Appli
48	370	10.6	915	2	US-09-905-125A-34	Sequence 34, Appli
49	370	10.6	915	2	US-09-902-775A-34	Sequence 34, Appli
50	370	10.6	915	2	US-09-906-700-34	Sequence 34, Appli
51	370	10.6	915	2	US-09-903-603A-34	Sequence 34, Appli
52	370	10.6	915	2	US-09-904-920A-34	Sequence 34, Appli
53	370	10.6	915	2	US-09-909-064-34	Sequence 34, Appli
54	370	10.6	915	2	US-09-905-381A-34	Sequence 34, Appli
55	370	10.6	915	2	US-09-906-618-34	Sequence 34, Appli
56	370	10.6	915	2	US-09-906-646-34	Sequence 34, Appli
57	370	10.6	915	2	US-09-904-462-34	Sequence 34, Appli
58	370	10.6	915	2	US-09-902-736A-34	Sequence 34, Appli
59	370	10.6	915	2	US-09-906-722A-34	Sequence 34, Appli
60	370	10.6	915	2	US-09-905-449-34	Sequence 34, Appli
61	370	10.6	915	2	US-09-903-562B-34	Sequence 34, Appli
62	370	10.6	915	2	US-09-906-679A-34	Sequence 34, Appli
63	370	10.6	915	3	US-09-907-841-34	Sequence 34, Appli
64	357.5	10.2	956	2	US-09-949-016-6215	Sequence 6215, Ap
65	357.5	10.2	953	2	US-09-949-016-11519	Sequence 11519, A
66	357.5	10.2	963	2	US-09-949-016-11550	Sequence 11550, A
67	356	10.2	969	3	US-10-000-512-10	Sequence 10, Appli
68	337.5	9.6	966	1	US-08-897-443-3	Sequence 3, Appli
69	336	9.6	145	3	US-09-394-264-4	Sequence 4, Appli
70	300	8.6	755	3	US-09-919-497-57	Sequence 57, Appli
71	290.5	8.3	954	2	US-09-996-611D-1	Sequence 1, Appli
72	283.5	8.1	171	2	US-09-996-611D-2	Sequence 2, Appli
73	268	7.7	149	3	US-09-394-264-8	Sequence 8, Appli
74	266	7.6	2050	1	US-08-347-594A-2	Sequence 2, Appli
75	266	7.6	2813	2	US-09-381-261A-1	Sequence 1, Appli
76	263.5	7.5	638	1	US-08-897-443-1	Sequence 1, Appli
77	263.5	7.5	776	3	US-10-000-512-8	Sequence 8, Appli
78	262	7.5	481	2	US-09-914-259-35	Sequence 35, Appli
79	251	7.2	466	2	US-09-914-259-35	Sequence 35, Appli
80	251	7.2	466	2	US-09-976-594-278	Sequence 278, App
81	251	7.2	466	2	US-09-949-016-9878	Sequence 9878, Ap
82	251	7.2	507	2	US-09-914-259-34	Sequence 34, Appli
83	248.5	7.1	442	2	US-08-896-449A-2	Sequence 2, Appli
84	243.5	7.0	2813	2	US-09-132-652-2	Sequence 2, Appli
85	243.5	7.0	2813	2	US-09-886-900A-2	Sequence 2, Appli
86	243.5	7.0	2813	2	US-09-662-478C-2	Sequence 2, Appli
87	243.5	7.0	2813	2	US-09-394-264-9	Sequence 9, Appli
88	233.5	6.7	145	3	US-09-394-264-9	Sequence 9, Appli
89	232	6.6	216	2	US-09-795-872-5	Sequence 5, Appli
90	232	6.6	405	2	US-09-112-283C-374	Sequence 374, App
91	231	6.6	187	1	US-08-177-109A-61	Sequence 61, Appli
92	231	6.6	187	1	US-08-687-106-61	Sequence 61, Appli
93	231	6.6	435	2	PCT-US95-04439-1	Sequence 1, Appli
94	231	6.6	1137	2	US-09-902-481B-5	Sequence 5, Appli
95	231	6.6	1152	1	US-08-476-062A-43	Sequence 43, Appli
96	231	6.6	1152	5	PCT-US96-01314-43	Sequence 43, Appli
97	231	6.6	1152	7	5424399-2	Patent No. 5424399
98	231	6.6	1153	1	US-08-173-497-3	Sequence 3, Appli
99	231	6.6	1153	1	US-08-286-889-3	Sequence 3, Appli

100	231	6.6	1153	1	US-08-485-618-3	Sequence 3, Appl1	173	203.5	5.8	1170	1	US-08-789-078-2	Sequence 2, Appl1
101	231	6.6	1153	1	US-08-362-652-3	Sequence 3, Appl1	174	203.5	5.8	1170	1	US-08-752-633-2	Sequence 2, Appl1
102	231	6.6	1153	1	US-08-605-672-3	Sequence 3, Appl1	175	203.5	5.8	1170	1	US-10-261-164-1	Sequence 1, Appl1
103	231	6.6	1153	1	US-08-482-293A-3	Sequence 3, Appl1	176	203.5	5.8	1170	5	PCT-US95-04886-2	Sequence 2, Appl1
104	231	6.6	1153	1	US-08-943-363-3	Sequence 3, Appl1	177	203.5	5.8	1180	2	US-09-000-004A-2	Sequence 2, Appl1
105	231	6.6	1153	2	US-09-193-043-3	Sequence 3, Appl1	178	203	5.8	184	2	US-08-974-899-7	Sequence 7, Appl1
106	231	6.6	1153	2	US-09-688-307A-3	Sequence 3, Appl1	179	203	5.8	184	2	US-09-795-798-7	Sequence 7, Appl1
107	231	6.6	1153	2	US-09-350-259-3	Sequence 3, Appl1	180	201.5	5.8	589	2	US-10-261-164-2	Sequence 2, Appl1
108	231	6.6	1153	2	US-09-902-481B-1	Sequence 1, Appl1	181	201.5	5.8	1065	2	US-08-630-1172-9	Sequence 9, Appl1
109	228	6.5	1163	1	US-08-476-062A-44	Sequence 4, Appl1	182	201.5	5.8	1065	2	US-09-375-412-9	Sequence 9, Appl1
110	228	6.5	1163	5	PCT-US96-01314-44	Sequence 4, Appl1	183	201.5	5.8	1170	5	US-08-476-062A-42	Sequence 4, Appl1
111	226	6.5	1137	2	US-09-902-481B-6	Sequence 6, Appl1	184	201.5	5.8	1170	5	PCT-US96-01314-42	Sequence 4, Appl1
112	226	6.4	1163	1	US-08-173-497-4	Sequence 4, Appl1	185	197	5.6	184	2	US-08-974-899-8	Sequence 8, Appl1
113	225	6.4	1163	1	US-08-286-889-4	Sequence 4, Appl1	186	197	5.6	184	2	US-09-795-798-8	Sequence 8, Appl1
114	225	6.4	1163	1	US-08-485-618-4	Sequence 4, Appl1	187	193.5	5.5	181	5	PCT-US96-01314-61	Sequence 8, Appl1
115	225	6.4	1163	1	US-08-362-652-4	Sequence 4, Appl1	188	192.5	5.5	1155	1	US-08-486-889-46	Sequence 6, Appl1
116	225	6.4	1163	1	US-08-605-672-4	Sequence 4, Appl1	189	192.5	5.5	1155	1	US-08-485-618-46	Sequence 4, Appl1
117	225	6.4	1163	1	US-08-482-293A-4	Sequence 4, Appl1	190	192.5	5.5	1155	1	US-08-362-652-46	Sequence 4, Appl1
118	225	6.4	1163	1	US-08-943-363-4	Sequence 4, Appl1	191	192.5	5.5	1155	1	US-08-605-672-46	Sequence 4, Appl1
119	225	6.4	1163	1	US-09-193-043-4	Sequence 4, Appl1	192	192.5	5.5	1155	1	US-08-482-293A-46	Sequence 4, Appl1
120	225	6.4	1163	2	US-09-688-307A-4	Sequence 4, Appl1	193	192.5	5.5	1155	1	US-08-943-363-46	Sequence 4, Appl1
121	225	6.4	1163	2	US-09-350-259-4	Sequence 4, Appl1	194	192.5	5.5	1155	2	US-09-193-043-46	Sequence 4, Appl1
122	223	6.4	187	1	US-08-177-109A-62	Sequence 62, Appl1	195	192.5	5.5	1155	2	US-09-688-307A-46	Sequence 4, Appl1
123	223	6.4	187	1	US-08-687-706-62	Sequence 62, Appl1	196	192.5	5.5	1155	2	US-09-350-259-46	Sequence 4, Appl1
124	223	6.4	187	5	PCT-US96-01314-60	Sequence 60, Appl1	197	192.5	5.5	1155	2	US-08-485-618-53	Sequence 5, Appl1
125	219.5	6.3	1161	1	US-08-173-497-2	Sequence 2, Appl1	198	192.5	5.5	1161	1	US-08-362-652-53	Sequence 5, Appl1
126	219.5	6.3	1161	1	US-08-286-889-2	Sequence 2, Appl1	199	192.5	5.5	1161	1	US-08-605-672-53	Sequence 5, Appl1
127	219.5	6.3	1161	1	US-08-485-618-2	Sequence 2, Appl1	200	192.5	5.5	1161	1	US-08-482-293A-53	Sequence 5, Appl1
128	219.5	6.3	1161	1	US-08-485-618-2	Sequence 2, Appl1	201	192.5	5.5	1161	1	US-08-943-363-53	Sequence 5, Appl1
129	219.5	6.3	1161	1	US-08-362-652-2	Sequence 2, Appl1	202	192.5	5.5	1161	2	US-09-193-043-53	Sequence 5, Appl1
130	219.5	6.3	1161	1	US-08-605-672-2	Sequence 2, Appl1	203	192.5	5.5	1161	2	US-09-688-307A-53	Sequence 5, Appl1
131	219.5	6.3	1161	1	US-08-605-672-2	Sequence 2, Appl1	204	192.5	5.5	1161	2	US-09-550-259-53	Sequence 5, Appl1
132	219.5	6.3	1161	1	US-08-482-293A-2	Sequence 2, Appl1	205	192.5	5.5	1217	2	US-09-949-016-7892	Sequence 6, Appl1
133	219.5	6.3	1161	1	US-08-482-293A-99	Sequence 99, Appl1	206	187	5.3	214	2	US-10-061-658-6	Sequence 6, Appl1
134	219.5	6.3	1161	1	US-08-943-363-2	Sequence 2, Appl1	207	187	5.3	214	2	US-10-061-658-9	Sequence 9, Appl1
135	219.5	6.3	1161	1	US-08-943-363-99	Sequence 99, Appl1	208	186	5.3	212	2	US-09-896-738A-6	Sequence 6, Appl1
136	219.5	6.3	1161	1	US-09-193-043-2	Sequence 2, Appl1	209	184.5	5.3	3571	2	US-09-911-842A-2	Sequence 2, Appl1
137	219.5	6.3	1161	2	US-09-193-043-99	Sequence 99, Appl1	210	182.5	5.2	1181	2	US-09-000-004A-2	Sequence 4, Appl1
138	219.5	6.3	1161	2	US-09-688-307A-2	Sequence 2, Appl1	211	182.5	5.2	1181	2	US-09-949-016-6189	Sequence 6189, Ap
139	219.5	6.3	1161	2	US-09-688-307A-99	Sequence 99, Appl1	212	182.5	5.2	1185	2	US-09-949-016-10747	Sequence 10747, A
140	219.5	6.3	1161	2	US-09-350-259-2	Sequence 2, Appl1	213	182.5	5.2	3594	2	US-09-911-842A-4	Sequence 4, Appl1
141	219.5	6.3	1161	2	US-09-350-259-99	Sequence 99, Appl1	214	179.5	5.1	1183	2	US-09-532-310B-6	Sequence 6, Appl1
142	219	6.3	1137	2	US-09-902-481B-4	Sequence 4, Appl1	215	175.5	5.0	1183	2	US-09-532-310B-5	Sequence 5, Appl1
143	214.5	6.1	413	1	US-08-485-618-101	Sequence 101, App	216	162.5	4.6	1178	1	US-08-199-776-2	Sequence 2, Appl1
144	214.5	6.1	413	1	US-08-605-672-101	Sequence 101, App	217	162.5	4.6	1178	2	US-08-673-731-2	Sequence 2, Appl1
145	214.5	6.1	413	1	US-08-482-293A-101	Sequence 101, App	218	162.5	4.6	1178	2	US-08-879-338-2	Sequence 2, Appl1
146	214.5	6.1	413	1	US-08-943-363-101	Sequence 101, App	219	162.5	4.6	1178	5	PCT-US95-0204A-2	Sequence 2, Appl1
147	214.5	6.1	413	2	US-09-688-307A-101	Sequence 101, App	220	162.5	4.6	1179	2	US-09-949-002-337	Sequence 337, App
148	214.5	6.1	413	2	US-09-350-259-101	Sequence 101, App	221	162.5	4.6	1179	2	US-09-949-002-503	Sequence 503, App
149	214.5	6.1	413	2	US-09-350-259-99	Sequence 99, Appl1	222	162.5	4.6	1214	2	US-08-996-014A-2	Sequence 2, Appl1
150	214	6.1	557	2	US-09-523-487-10	Sequence 10, Appl1	223	160	4.6	1083	1	US-08-596-405-2	Sequence 2, Appl1
151	214	6.1	557	1	US-08-286-889-37	Sequence 37, Appl1	224	160	4.6	1083	1	US-08-877-620-2	Sequence 2, Appl1
152	212.5	6.1	1151	2	US-08-485-618-37	Sequence 37, Appl1	225	160	4.6	1083	2	US-09-287-368-2	Sequence 2, Appl1
153	212.5	6.1	1151	1	US-08-362-652-37	Sequence 37, Appl1	226	160	4.6	1083	2	US-09-626-799-2	Sequence 2, Appl1
154	212.5	6.1	1151	1	US-08-605-672-37	Sequence 37, Appl1	227	160	4.6	1083	2	US-10-183-992-6	Sequence 6, Appl1
155	212.5	6.1	1151	1	US-08-482-293A-37	Sequence 37, Appl1	228	160	4.6	498	2	US-08-183-992-2	Sequence 2, Appl1
156	212.5	6.1	1151	1	US-08-943-363-37	Sequence 37, Appl1	229	159.5	4.6	1019	1	US-08-996-014A-4	Sequence 4, Appl1
157	212.5	6.1	1151	2	US-09-193-043-37	Sequence 37, Appl1	230	159.5	4.6	1019	1	US-08-877-620-4	Sequence 4, Appl1
158	212.5	6.1	1151	2	US-09-688-307A-37	Sequence 37, Appl1	231	159.5	4.6	1019	1	US-08-877-620-4	Sequence 4, Appl1
159	212.5	6.1	1151	2	US-09-350-259-37	Sequence 37, Appl1	232	159.5	4.6	1019	2	US-09-287-368-4	Sequence 4, Appl1
160	212.5	6.1	1151	2	US-08-485-618-55	Sequence 55, Appl1	233	159.5	4.6	1019	2	US-09-626-799-2	Sequence 2, Appl1
161	212.5	6.1	1161	1	US-08-362-652-55	Sequence 55, Appl1	234	159.5	4.6	1019	2	US-10-183-992-4	Sequence 4, Appl1
162	212.5	6.1	1161	1	US-08-605-672-55	Sequence 55, Appl1	235	159.5	4.6	1019	2	US-08-877-620-4	Sequence 4, Appl1
163	212.5	6.1	1161	1	US-08-482-293A-55	Sequence 55, Appl1	236	157.5	4.5	1019	2	US-08-943-363-93	Sequence 93, Appl1
164	212.5	6.1	1161	1	US-08-943-363-55	Sequence 55, Appl1	237	157.5	4.5	264	1	US-08-362-652-93	Sequence 93, Appl1
165	212.5	6.1	1161	1	US-08-943-363-55	Sequence 55, Appl1	238	157.5	4.5	264	1	US-08-362-652-93	Sequence 93, Appl1
166	212.5	6.1	1161	2	US-09-193-043-55	Sequence 55, Appl1	239	157.5	4.5	264	1	US-08-605-672-93	Sequence 93, Appl1
167	212.5	6.1	1161	2	US-09-688-307A-55	Sequence 55, Appl1	240	157.5	4.5	264	1	US-08-482-293A-93	Sequence 93, Appl1
168	212.5	6.1	1161	2	US-09-350-259-55	Sequence 55, Appl1	241	157.5	4.5	264	1	US-08-943-363-93	Sequence 93, Appl1
169	211	6.0	105	3	US-09-394-264-11	Sequence 11, Appl1	242	157.5	4.5	264	2	US-09-193-043-93	Sequence 93, Appl1
170	208	5.9	1137	2	US-09-902-481B-3	Sequence 3, Appl1	243	157.5	4.5	264	2	US-09-688-307A-93	Sequence 93, Appl1
171	205	5.9	214	2	US-10-061-658-5	Sequence 5, Appl1	244	157.5	4.5	264	2	US-09-350-259-93	Sequence 93, Appl1
172	204	5.8	212	2	US-09-996-738A-5	Sequence 5, Appl1	245	149.5	4.3	1132	3	US-09-647-544A-5	Sequence 5, Appl1

246	149.5	4.3	1167	2	US-09-949-002-355	Sequence 355, App	319	108	3.1	538	2	US-09-976-740-43	Sequence 43, Appl
247	149.5	4.3	1167	3	US-09-647-544A-4	Sequence 4, Appl1	320	108	3.1	695	1	US-08-164-839-8	Sequence 8, Appl1
248	149.5	4.3	1174	2	US-09-949-002-511	Sequence 511, App	321	108	3.1	695	1	US-08-583-799-8	Sequence 8, Appl1
249	144	4.1	137	2	US-09-394-264-10	Sequence 10, Appl	322	108	3.1	666	1	US-08-164-839-10	Sequence 10, Appl
250	143.5	4.1	500	2	US-09-999-833A-363	Sequence 363, App	323	108	3.1	666	1	US-08-583-799-10	Sequence 10, Appl
251	143.5	4.1	500	2	US-10-020-445A-363	Sequence 363, App	324	108	3.1	666	1	US-09-504-987-5	Sequence 5, Appl1
252	143.5	4.1	500	2	US-09-978-189-563	Sequence 363, App	325	108	3.1	758	2	US-09-949-016-6695	Sequence 6695, Ap
253	143.5	4.1	500	2	US-10-017-085A-363	Sequence 363, App	326	108	3.1	998	2	US-09-949-016-6695	Sequence 8112, Ap
254	143.5	4.1	500	3	US-10-145-129A-363	Sequence 363, App	327	108	3.1	1377	2	US-09-949-016-8412	Sequence 33, Appl
255	143.5	4.1	500	3	US-10-013-929A-363	Sequence 363, App	328	107	3.1	517	2	US-10-152-886-33	Sequence 3115, A
256	143.5	4.1	500	3	US-10-013-917A-363	Sequence 363, App	329	107	3.1	550	2	US-09-616-289-47	Sequence 47, Appl
257	140	4.0	503	2	US-09-823-038A-51	Sequence 51, Appl	330	107	3.1	550	2	US-09-976-740-47	Sequence 47, Appl
258	137.5	3.9	320	1	US-07-841-551A-15	Sequence 15, Appl	331	106.5	3.0	1307	2	US-10-104-047-2438	Sequence 2438, Ap
259	137.5	3.9	320	5	PCT-US93-02034-15	Sequence 15, Appl	332	106	3.0	660	2	US-09-462-606-57	Sequence 57, Appl
260	133.5	3.8	487	2	US-09-691-344A-2	Sequence 2, Appl	333	106	3.0	1130	2	US-09-442-100-4	Sequence 4, Appl1
261	133.5	3.8	539	2	US-09-691-344A-6	Sequence 6, Appl1	334	106	3.0	1130	2	US-09-333-857-3	Sequence 3, Appl1
262	133.5	3.8	586	2	US-09-691-344A-4	Sequence 4, Appl1	335	106	3.0	1130	2	US-08-939-106-4	Sequence 4, Appl1
263	131.5	3.8	187	2	US-08-463-682-1	Sequence 1, Appl1	336	106	3.0	1130	2	US-09-442-100-4	Sequence 4, Appl1
264	131.5	3.8	220	2	US-08-463-682-24	Sequence 24, Appl	337	106	3.0	1130	2	US-09-442-100-4	Sequence 4, Appl1
265	131.5	3.8	225	2	US-08-463-682-23	Sequence 23, Appl	338	105.5	3.0	487	2	US-09-949-016-6536	Sequence 6536, Ap
266	131.5	3.8	226	1	US-08-347-594A-4	Sequence 4, Appl1	339	105.5	3.0	577	2	US-09-328-352-7698	Sequence 10469, A
267	131.5	3.8	247	1	US-08-797-689-4	Sequence 4, Appl1	340	105.5	3.0	826	1	US-07-638-431-2	Sequence 7698, Ap
268	131.5	3.8	247	2	US-09-984-186-4	Sequence 4, Appl1	341	105.5	3.0	826	5	PCT-US92-00018-2	Sequence 2, Appl1
269	131.5	3.8	247	2	US-10-237-866-4	Sequence 4, Appl1	342	105.5	3.0	867	1	US-07-867-106-3	Sequence 2, Appl1
270	131.5	3.8	247	2	US-10-702-636-4	Sequence 4, Appl1	343	105.5	3.0	1738	2	US-08-486-049-2	Sequence 3, Appl1
271	131.5	3.8	247	2	US-10-702-636-4	Sequence 4, Appl1	344	105.5	3.0	1738	2	US-10-314-739A-2	Sequence 2, Appl1
272	129	3.7	492	2	US-10-104-047-3481	Sequence 3481, Ap	345	105	3.0	478	2	US-09-902-540-14070	Sequence 14070, A
273	126.5	3.6	554	2	US-10-094-749-2500	Sequence 2500, Ap	346	105	3.0	568	2	US-09-902-540-10388	Sequence 10388, A
274	126.5	3.6	775	2	US-10-191-436A-2	Sequence 2, Appl1	347	105	3.0	927	3	US-09-543-681A-6566	Sequence 6566, Ap
275	125.5	3.6	827	2	US-09-248-796A-17307	Sequence 17307, A	348	105	3.0	927	3	US-10-069-799-5	Sequence 5, Appl1
276	125	3.6	226	2	US-08-463-682-5	Sequence 5, Appl1	349	105	3.0	1190	2	US-09-252-991A-21474	Sequence 21474, A
277	125	3.6	769	2	US-10-191-436A-8	Sequence 8, Appl1	350	104.5	3.0	1456	1	US-08-803-973-2	Sequence 2, Appl1
278	124.5	3.6	921	1	US-09-136-574A-43	Sequence 43, Appl	351	104.5	3.0	786	2	US-08-103-4292-3	Sequence 2, Appl1
279	124.5	3.6	921	1	US-08-818-823-2	Sequence 2, Appl1	352	104	3.0	786	2	US-09-294-663-3	Sequence 3, Appl1
280	124.5	3.6	921	1	US-08-818-823-2	Sequence 2, Appl1	353	104	3.0	788	2	US-09-294-663-3	Sequence 3, Appl1
281	124.5	3.6	1171	2	US-09-417-197-131	Sequence 11, App	354	104	3.0	1018	2	US-10-090-827-13	Sequence 13, Appl
282	124.5	3.6	1181	2	US-09-417-197-133	Sequence 13, App	355	104	3.0	1018	2	US-09-397-548-15	Sequence 15, Appl
283	124	3.5	769	2	US-10-191-436A-5	Sequence 5, Appl1	356	104	3.0	1036	2	US-10-090-827-14	Sequence 14, Appl
284	122.5	3.5	1638	2	US-09-071-035-258	Sequence 258, App	357	104	3.0	1036	2	US-09-397-548-16	Sequence 16, Appl
285	122.5	3.5	1638	2	US-09-071-035-262	Sequence 262, App	358	104	3.0	1063	2	US-10-090-827-15	Sequence 15, Appl
286	122.5	3.5	1638	2	US-09-071-035-266	Sequence 266, App	359	104	3.0	1063	2	US-09-397-548-17	Sequence 17, Appl
287	122.5	3.5	1638	2	US-10-206-576-258	Sequence 258, App	360	104	3.0	1079	1	US-08-455-543A-55	Sequence 55, Appl
288	122.5	3.5	1638	2	US-10-206-576-262	Sequence 262, App	361	104	3.0	1079	1	US-08-223-305C-55	Sequence 55, Appl
289	122.5	3.5	1638	2	US-10-206-576-266	Sequence 266, App	362	104	3.0	1084	1	US-08-455-543A-56	Sequence 56, Appl
290	122.5	3.5	1747	2	US-09-134-000C-55999	Sequence 5999, Ap	363	104	3.0	1084	1	US-08-223-305C-56	Sequence 56, Appl
291	121.5	3.5	903	2	US-09-623-624-18	Sequence 18, Appl	364	104	3.0	1086	1	US-08-455-543A-54	Sequence 54, Appl
292	121.5	3.5	903	2	US-10-270-595-18	Sequence 18, Appl	365	104	3.0	1086	1	US-08-223-305C-54	Sequence 54, Appl
293	120.5	3.4	903	2	US-09-193-562D-46	Sequence 46, Appl	366	104	3.0	1091	1	US-07-745-206A-25	Sequence 25, Appl
294	120.5	3.4	903	2	US-10-055-412B-46	Sequence 46, Appl	367	104	3.0	1091	1	US-08-455-543A-52	Sequence 52, Appl
295	115.5	3.3	538	1	US-08-541-759B-2	Sequence 2, Appl1	368	104	3.0	1091	1	US-08-223-305C-52	Sequence 25, Appl
296	115.5	3.3	772	2	US-09-252-991A-30446	Sequence 30446, A	369	104	3.0	1091	1	US-08-111-363-25	Sequence 4, Appl1
297	115.5	3.3	1050	2	US-09-045-632-50	Sequence 50, Appl	370	104	3.0	1091	2	US-08-713-118-4	Sequence 4, Appl1
298	113.5	3.2	835	2	US-09-949-016-7974	Sequence 7974, Ap	371	104	3.0	1091	2	US-09-452-007-4	Sequence 17, Appl
299	112.5	3.2	1050	2	US-09-045-632-49	Sequence 49, Appl	372	104	3.0	1091	2	US-10-162-012-17	Sequence 17, Appl
300	112	3.2	536	2	US-09-292-225-21	Sequence 21, Appl	373	104	3.0	1091	2	US-10-090-827-16	Sequence 16, Appl
301	112	3.2	555	2	US-09-292-225-15	Sequence 15, Appl	374	104	3.0	1091	2	US-09-397-548-14	Sequence 14, Appl
302	112	3.2	555	2	US-09-292-225-18	Sequence 18, Appl	375	104	3.0	1091	2	US-09-397-548-14	Sequence 14, Appl
303	111.5	3.2	490	2	US-10-029-180-76	Sequence 76, Appl	376	104	3.0	1103	1	US-08-455-543A-53	Sequence 53, Appl
304	111.5	3.2	910	2	US-09-902-540-10793	Sequence 10793, A	377	103.5	3.0	616	2	US-08-223-305C-53	Sequence 53, Appl
305	111	3.2	434	2	US-09-252-991A-26737	Sequence 26737, A	378	103.5	3.0	660	2	US-09-136-574A-47	Sequence 47, Appl
306	111	3.2	795	2	US-09-193-562D-11	Sequence 11, Appl	379	103.5	3.0	660	2	US-09-462-606-53	Sequence 53, Appl
307	111	3.2	795	2	US-10-055-412B-11	Sequence 11, Appl	380	103	2.9	568	2	US-09-543-681A-7677	Sequence 7677, Ap
308	111	3.2	821	2	US-09-193-562D-12	Sequence 12, Appl	381	102.5	2.9	266	2	US-09-252-991A-17693	Sequence 17693, A
309	111	3.2	821	2	US-10-055-412B-12	Sequence 12, Appl	382	102.5	2.9	660	2	US-09-489-847-332	Sequence 332, A
310	111	3.2	905	2	US-09-193-562D-2	Sequence 2, Appl1	383	102.5	2.9	661	2	US-09-462-606-47	Sequence 47, Appl
311	111	3.2	905	2	US-10-055-412B-2	Sequence 2, Appl1	384	102.5	2.9	669	2	US-09-328-352-6748	Sequence 6748, Ap
312	110	3.1	558	2	US-09-071-035-268	Sequence 268, App	385	102.5	2.9	669	2	US-09-071-035-264	Sequence 264, App
313	110	3.1	558	2	US-10-206-576-268	Sequence 268, App	386	102.5	2.9	784	2	US-10-206-576-264	Sequence 264, Appl
314	110	3.1	1367	2	US-09-487-558B-108	Sequence 108, App	387	102.5	2.9	784	2	US-09-967-805-7	Sequence 7, Appl1
315	109	3.1	488	2	US-10-104-047-2639	Sequence 2639, Ap	388	102.5	2.9	784	2	US-09-967-805-7	Sequence 7, Appl1
316	109	3.1	533	2	US-09-270-767-42903	Sequence 42903, A	389	102.5	2.9	805	2	US-10-631-407A-7	Sequence 7, Appl1
317	109	3.1	2385	2	US-09-543-681A-6304	Sequence 6304, Ap	390	102.5	2.9	807	2	US-09-103-429A-4	Sequence 4, Appl1
318	108	3.1	538	2	US-09-616-289-43	Sequence 43, Appl	391	102.5	2.9	4630	2	US-09-294-663-4	Sequence 2, Appl1

392	102.5	2.9	5215	2	US-09-105-537-2	Sequence 2, Appl1	465	99.5	2.8	1971	2	US-09-854-856-32	Sequence 32, Appl1
393	102	2.9	632	2	US-09-354-129-8	Sequence 8, Appl1	466	99.5	2.8	1971	2	US-10-010-720-32	Sequence 32, Appl1
394	102	2.9	632	2	US-09-504-357-8	Sequence 8, Appl1	467	99.5	2.8	1971	2	US-09-854-856-16	Sequence 16, Appl1
395	102	2.9	825	2	US-09-270-767-45321	Sequence 45321, A	468	99.5	2.8	1999	2	US-10-010-720-16	Sequence 16, Appl1
396	102	2.9	1086	7	5386025-8	Patent No. 5386025	469	99.5	2.8	2048	2	US-09-854-856-62	Sequence 62, Appl1
397	102	2.9	1721	2	US-08-700-651-5	Sequence 5, Appl1	470	99.5	2.8	2048	2	US-10-010-720-62	Sequence 62, Appl1
398	102	2.9	1721	2	US-08-928-561B-6	Sequence 6, Appl1	471	99.5	2.8	2076	2	US-09-854-856-46	Sequence 46, Appl1
399	102	2.9	1721	2	US-09-588-995A-6	Sequence 6, Appl1	472	99.5	2.8	2076	2	US-10-010-720-46	Sequence 46, Appl1
400	102	2.9	2441	1	US-08-194-468-2	Sequence 2, Appl1	473	99.5	2.8	2108	2	US-09-854-856-30	Sequence 30, Appl1
401	102	2.9	2441	2	US-08-961-739-2	Sequence 2, Appl1	474	99.5	2.8	2108	2	US-10-010-720-30	Sequence 30, Appl1
402	102	2.9	2441	2	US-09-514-247A-8	Sequence 8, Appl1	475	99.5	2.8	2136	2	US-09-854-856-14	Sequence 14, Appl1
403	102	2.9	2441	2	US-09-686-316-2	Sequence 2, Appl1	476	99.5	2.8	2136	2	US-10-010-720-14	Sequence 14, Appl1
404	101.5	2.9	660	2	US-09-462-606-54	Sequence 54, Appl1	477	99	2.8	525	2	US-08-542-634-27	Sequence 27, Appl1
405	101.5	2.9	809	2	US-09-949-016-9974	Sequence 9974, Ap	478	99	2.8	525	2	PCT-US95-13703-27	Sequence 27, Appl1
406	101.5	2.9	1093	2	US-08-545-860D-55	Sequence 55, Appl1	479	99	2.8	540	5	US-08-542-634-25	Sequence 25, Appl1
407	101.5	2.9	1093	5	PCT-US94-04496-55	Sequence 55, Appl1	480	99	2.8	540	5	PCT-US95-13703-25	Sequence 25, Appl1
408	101.5	2.9	1335	3	US-09-134-001C-3716	Sequence 3716, Ap	481	99	2.8	549	2	US-08-542-634-15	Sequence 15, Appl1
409	101.5	2.9	1713	3	US-10-114-270-194	Sequence 194, Ap	482	99	2.8	549	2	US-08-477-292-15	Sequence 15, Appl1
410	101.5	2.9	1848	2	US-08-296-791-6	Sequence 6, Appl1	483	99	2.8	549	5	PCT-US95-13703-15	Sequence 15, Appl1
411	101.5	2.9	1848	2	US-09-839-396-6	Sequence 6, Appl1	484	99	2.8	660	1	US-08-240-049B-15	Sequence 15, Appl1
412	101.5	2.9	1848	2	US-10-080-505-6	Sequence 6, Appl1	485	99	2.8	660	1	US-08-259-148A-19	Sequence 19, Appl1
413	101.5	2.9	1848	2	US-10-645-655-6	Sequence 6, Appl1	486	99	2.8	660	1	US-08-484-054-19	Sequence 19, Appl1
414	101.5	2.9	1848	3	US-10-687-046-6	Sequence 6, Appl1	487	99	2.8	660	1	US-07-876-941A-19	Sequence 19, Appl1
415	101.5	2.9	1848	5	PCT-US95-10661A-6	Sequence 6, Appl1	488	99	2.8	660	2	US-08-478-507-8	Sequence 8, Appl1
416	101.5	2.9	2157	2	US-09-854-856-52	Sequence 52, Appl1	489	99	2.8	660	2	US-08-542-634-13	Sequence 13, Appl1
417	101.5	2.9	2157	2	US-10-010-720-52	Sequence 52, Appl1	490	99	2.8	660	2	US-09-128-275A-8	Sequence 8, Appl1
418	101.5	2.9	2245	2	US-09-854-856-50	Sequence 50, Appl1	491	99	2.8	660	2	US-08-477-292-13	Sequence 13, Appl1
419	101.5	2.9	2185	2	US-10-010-720-36	Sequence 36, Appl1	492	99	2.8	660	2	US-09-553-427-8	Sequence 8, Appl1
420	101.5	2.9	2217	2	US-09-854-856-20	Sequence 20, Appl1	493	99	2.8	660	2	US-09-462-606-50	Sequence 50, Appl1
421	101.5	2.9	2217	2	US-10-010-720-20	Sequence 20, Appl1	494	99	2.8	660	2	US-07-870-985A-19	Sequence 19, Appl1
422	101.5	2.9	2245	2	US-09-854-856-4	Sequence 4, Appl1	495	99	2.8	660	2	PCT-US95-13703-19	Sequence 19, Appl1
423	101.5	2.9	2245	2	US-10-010-720-4	Sequence 4, Appl1	496	99	2.8	660	5	US-09-270-767-453B9	Sequence 453B9, A
424	101.5	2.9	2294	2	US-09-854-856-50	Sequence 50, Appl1	497	99	2.8	749	2	US-09-086-436-39	Sequence 39, Appl1
425	101.5	2.9	2294	2	US-09-854-856-50	Sequence 50, Appl1	498	99	2.8	1477	2	US-09-482-500A-1	Sequence 1, Appl1
426	101.5	2.9	2322	2	US-09-854-856-34	Sequence 34, Appl1	499	99	2.8	1704	2	US-08-336-308A-10	Sequence 10, Appl1
427	101.5	2.9	2322	2	US-10-010-720-34	Sequence 34, Appl1	500	99	2.8	1704	2	US-08-822-324-6	Sequence 6, Appl1
428	101.5	2.9	2354	2	US-09-854-856-18	Sequence 18, Appl1	501	99	2.8	1704	2	US-09-490-931-10	Sequence 10, Appl1
429	101.5	2.9	2354	2	US-10-010-720-18	Sequence 18, Appl1	502	99	2.8	1751	2	US-09-136-574A-44	Sequence 44, Appl1
430	101.5	2.9	2382	2	US-09-854-856-2	Sequence 2, Appl1	503	99	2.8	2972	2	US-09-579-181-2	Sequence 2, Appl1
431	101.5	2.9	2382	2	US-10-010-720-2	Sequence 2, Appl1	504	99	2.8	3118	2	US-09-579-181-1	Sequence 1, Appl1
432	101	2.9	482	2	US-09-252-991A-22658	Sequence 22658, A	505	98.5	2.8	460	2	US-09-949-016-8029	Sequence 8029, Ap
433	101	2.9	535	2	US-09-949-016-10290	Sequence 10290, A	506	98.5	2.8	661	1	US-08-417-174-27	Sequence 27, Appl1
434	101	2.9	724	2	US-09-900-920-62	Sequence 62, Appl1	507	98.5	2.8	661	1	US-08-417-174-121	Sequence 121, App
435	101	2.9	758	2	US-09-902-540-10176	Sequence 10176, A	508	98.5	2.8	661	1	US-08-331-565A-27	Sequence 27, Appl1
436	101	2.9	843	1	US-09-336-257A-8	Sequence 8, Appl1	509	98.5	2.8	661	1	US-09-007-961-27	Sequence 27, Appl1
437	100.5	2.9	1106	2	US-09-543-681A-6880	Sequence 6880, Ap	510	98.5	2.8	661	2	US-09-267-439-27	Sequence 27, Appl1
438	100.5	2.9	1296	2	US-08-470-260-3	Sequence 3, Appl1	511	98.5	2.8	661	2	US-09-267-439-121	Sequence 121, App
439	100.5	2.9	1296	2	US-08-471-491-3	Sequence 3, Appl1	512	98.5	2.8	661	2	US-08-388-852B-12	Sequence 2, Appl1
440	100.5	2.9	1296	2	US-08-466-662-3	Sequence 3, Appl1	513	98.5	2.8	661	2	US-09-073-138-27	Sequence 27, Appl1
441	100.5	2.9	1543	2	US-09-904-987-7	Sequence 7, Appl1	514	98.5	2.8	661	2	US-09-073-138-121	Sequence 121, App
442	100.5	2.9	3144	1	US-08-457-273B-42	Sequence 42, Appl1	515	98.5	2.8	661	2	US-09-862-260A-121	Sequence 2, Appl1
443	100.5	2.9	3144	2	US-08-556-419-21	Sequence 21, Appl1	516	98.5	2.8	661	2	US-09-898-860-27	Sequence 27, Appl1
444	100.5	2.9	3144	2	US-09-041-886-15	Sequence 15, Appl1	517	98.5	2.8	661	2	US-09-898-860-121	Sequence 121, App
445	100.5	2.9	3144	2	US-09-538-092-1118	Sequence 1118, Ap	518	98.5	2.8	668	2	US-08-993-010-2	Sequence 2, Appl1
446	100	2.9	234	2	US-09-476-202A-2	Sequence 2, Appl1	519	98.5	2.8	673	2	US-09-196-387-8	Sequence 8, Appl1
447	100	2.9	310	2	US-09-252-991A-23384	Sequence 23384, A	520	98.5	2.8	673	2	US-09-841-835-8	Sequence 8, Appl1
448	100	2.9	368	2	US-09-949-002-361	Sequence 8818, Ap	521	98.5	2.8	949	2	US-09-196-387-10	Sequence 10, Appl1
449	100	2.9	483	2	US-09-134-000C-4852	Sequence 4862, Ap	522	98.5	2.8	949	2	US-09-841-835-10	Sequence 10, Appl1
450	100	2.9	712	2	US-09-252-991A-21481	Sequence 21481, A	523	98.5	2.8	1181	2	US-09-703-809A-4	Sequence 4, Appl1
451	100	2.9	712	2	US-09-543-681A-6132	Sequence 6132, Ap	524	98.5	2.8	1327	2	US-09-196-387-2	Sequence 2, Appl1
452	100	2.9	1006	2	US-09-023-905A-12	Sequence 12, Appl1	525	98.5	2.8	1327	2	US-09-841-835-2	Sequence 2, Appl1
453	100	2.9	1006	2	US-09-949-002-361	Sequence 361, App	526	98.5	2.8	1327	2	US-09-972-115A-8	Sequence 8, Appl1
454	100	2.9	1207	2	US-09-252-991A-27473	Sequence 27470, A	527	98.5	2.8	1765	2	US-09-949-002-545	Sequence 545, App
455	100	2.9	3031	1	US-07-689-008-2	Sequence 2, Appl1	528	98.5	2.8	3241	2	US-09-841-786-1	Sequence 1, Appl1
456	99.5	2.8	268	2	US-10-104-047-1172	Sequence 3172, Ap	529	98	2.8	331	1	US-08-997-080-182	Sequence 182, App
457	99.5	2.8	383	2	US-09-252-991A-29621	Sequence 29621, A	530	98	2.8	331	1	US-08-997-362-182	Sequence 182, App
458	99.5	2.8	660	2	US-09-462-606-56	Sequence 56, Appl1	531	98	2.8	331	2	US-09-095-855-182	Sequence 182, App
459	99.5	2.8	1182	2	US-09-336-529-4	Sequence 4, Appl1	532	98	2.8	331	2	US-09-324-542-182	Sequence 182, App
460	99.5	2.8	1744	2	US-09-438-185A-542	Sequence 542, App	533	98	2.8	331	2	US-09-205-426-182	Sequence 182, App
461	99.5	2.8	1911	2	US-09-854-856-64	Sequence 64, Appl1	534	98	2.8	378	2	US-09-949-016-7408	Sequence 7408, Ap
462	99.5	2.8	1911	2	US-10-010-720-64	Sequence 64, Appl1	535	98	2.8	390	2	US-09-252-991A-26543	Sequence 26543, A
463	99.5	2.8	1939	2	US-09-854-856-68	Sequence 48, Appl1	536	98	2.8	559	1	US-08-313-288B-14	Sequence 14, Appl1
464	99.5	2.8	1939	2	US-10-010-720-48	Sequence 48, Appl1	537	98	2.8	749	2	US-08-997-688A-10	Sequence 10, Appl1

538	98	2.8	788	2	US-09-489-039A-11122	Sequence 11122, A	611	95	2.7	1041	2	US-09-270-767-32619	Sequence 32619, A
539	98	2.8	962	2	US-09-442-100-6	Sequence 6, Appl1	612	95	2.7	1041	2	US-09-270-767-47836	Sequence 47836, A
540	98	2.8	962	2	US-08-939-106-6	Sequence 6, Appl1	613	95	2.7	1063	2	US-09-595-8578-29	Sequence 29, Appl1
541	98	2.8	962	2	US-09-442-102-6	Sequence 6, Appl1	614	95	2.7	1098	1	US-08-290-301-82	Sequence 82, Appl1
542	98	2.8	1106	1	US-08-435-675B-5	Sequence 5, Appl1	615	95	2.7	1098	2	US-09-013-598-82	Sequence 82, Appl1
543	97.5	2.8	371	2	US-09-252-991A-2868	Sequence 2868, A	616	95	2.7	1118	2	US-09-270-767-2	Sequence 2, Appl1
544	97.5	2.8	508	1	US-08-435-675B-6	Sequence 6, Appl1	617	95	2.7	1118	2	US-09-270-767-42703	Sequence 42703, A
545	97.5	2.8	614	2	US-09-830-902-107	Sequence 107, Appl	618	95	2.7	1118	2	US-09-270-767-43454	Sequence 43454, A
546	97.5	2.8	660	2	US-09-462-606-12	Sequence 12, Appl	619	95	2.7	1184	2	US-09-266-225D-18	Sequence 18, Appl
547	97.5	2.8	660	2	US-09-462-606-51	Sequence 51, Appl	620	95	2.7	1185	2	US-09-041-886-23	Sequence 23, Appl
548	97.5	2.8	668	1	US-07-891-942G-6	Sequence 6, Appl1	621	95	2.7	1185	2	US-09-538-092-1209	Sequence 1209, Ap
549	97.5	2.8	720	2	US-09-710-279-2058	Sequence 2058, Ap	622	95	2.7	2189	2	US-10-172-502-2	Sequence 2, Appl1
550	97.5	2.8	728	2	US-09-134-001C-4968	Sequence 4968, Ap	623	94.5	2.7	206	2	US-09-252-991A-24085	Sequence 24085, A
551	97.5	2.8	860	2	US-09-781-693A-3	Sequence 3, Appl1	624	94.5	2.7	289	2	US-09-216-933B-92	Sequence 92, Appl1
552	97	2.8	281	1	US-08-040-548-3	Sequence 3, Appl1	625	94.5	2.7	447	1	US-08-450-360-4	Sequence 4, Appl1
553	97	2.8	384	2	US-08-466-344-3	Sequence 3, Appl1	626	94.5	2.7	483	1	US-09-949-016-11633	Sequence 11633, A
554	97	2.8	496	1	US-09-825-414-54	Sequence 54, Appl1	627	94.5	2.7	486	2	US-08-450-360-2	Sequence 2, Appl1
555	97	2.8	533	1	US-08-224-482-2	Sequence 2, Appl1	628	94.5	2.7	601	2	US-09-270-767-45496	Sequence 45496, A
556	97	2.8	533	1	US-08-040-548-1	Sequence 1, Appl1	629	94.5	2.7	699	2	US-10-237-551-143	Sequence 143, Ap
557	97	2.8	533	1	US-08-466-344-1	Sequence 1, Appl1	630	94.5	2.7	747	2	US-09-328-352-7649	Sequence 254, Ap
558	97	2.8	533	2	US-09-546-013-21	Sequence 21, Appl1	631	94.5	2.7	876	2	US-09-487-558B-44	Sequence 7649, Ap
559	97	2.8	533	7	5206152-2	Patent No. 5206152	632	94.5	2.7	941	2	US-09-487-558B-44	Sequence 44, Appl
560	97	2.8	807	2	US-09-438-185A-882	Sequence 882, Ap	633	94.5	2.7	941	2	US-07-757-022B-14	Sequence 14, Appl
561	97	2.8	1784	2	US-09-040-738-2	Sequence 2, Appl1	634	94.5	2.7	1022	3	US-10-124-557-14	Sequence 14, Appl
562	97	2.8	1784	2	US-08-652-426A-2	Sequence 2, Appl1	635	94.5	2.7	1022	3	US-07-757-022B-84	Sequence 84, Appl
563	97	2.8	2442	2	US-09-514-247A-10	Sequence 10, Appl	636	94.5	2.7	1028	2	US-10-124-557-84	Sequence 84, Appl
564	97	2.8	2442	2	US-09-538-092-1370	Sequence 1370, Ap	637	94.5	2.7	1028	2	US-07-757-022B-74	Sequence 74, Appl
565	96.5	2.8	533	1	US-08-225-488-2	Sequence 2, Appl1	638	94.5	2.7	1038	3	US-10-124-557-74	Sequence 74, Appl
566	96.5	2.8	542	2	US-09-538-092-289	Sequence 289, Ap	639	94.5	2.7	1039	2	US-07-757-022B-58	Sequence 58, Appl
567	96.5	2.8	668	1	US-09-277-431A-2	Sequence 2, Appl1	640	94.5	2.7	1099	3	US-10-124-557-58	Sequence 58, Appl
568	96.5	2.8	764	1	US-08-177-109A-2	Sequence 2, Appl1	641	94.5	2.7	1140	3	US-07-757-022B-104	Sequence 104, Ap
569	96.5	2.8	764	1	US-08-687-706-2	Sequence 2, Appl1	642	94.5	2.7	1140	3	US-10-124-557-104	Sequence 104, Ap
570	96.5	2.8	764	2	US-09-949-002-325	Sequence 325, Ap	643	94.5	2.7	1200	2	US-10-094-749-2682	Sequence 2682, Ap
571	96.5	2.8	798	2	US-09-949-016-11021	Sequence 11021, A	644	94.5	2.7	1270	2	US-07-757-022B-44	Sequence 44, Appl
572	96.5	2.8	798	2	US-09-447-389-2	Sequence 544, Ap	645	94.5	2.7	1270	3	US-10-124-557-44	Sequence 44, Appl
573	96.5	2.8	860	2	US-09-418-710-13	Sequence 2, Appl1	646	94.5	2.7	1306	2	US-09-538-092-330	Sequence 330, Ap
574	96.5	2.8	1878	2	US-09-839-479-13	Sequence 13, Appl	647	94.5	2.7	1311	2	US-07-757-022B-42	Sequence 42, Appl
575	96.5	2.8	1878	2	US-08-246-982A-6	Sequence 6, Appl1	648	94.5	2.7	1313	3	US-10-124-557-42	Sequence 42, Appl
576	96.5	2.8	3144	1	US-08-453-265-6	Sequence 6, Appl1	649	94.5	2.7	1313	3	US-07-757-022B-142	Sequence 142, Ap
577	96.5	2.8	430	2	US-09-252-991A-29287	Sequence 29287, A	650	94.5	2.7	1313	3	US-10-124-557-142	Sequence 142, Ap
578	96	2.7	437	2	US-09-949-016-8094	Sequence 8094, Ap	651	94.5	2.7	1314	2	US-07-757-022B-50	Sequence 50, Appl
579	96	2.7	552	2	US-09-112-699-16	Sequence 16, Appl	652	94.5	2.7	1314	3	US-10-124-557-50	Sequence 50, Appl
580	96	2.7	561	2	US-09-172-699-20	Sequence 20, Appl	653	94.5	2.7	1330	2	US-07-757-022B-46	Sequence 46, Appl
581	96	2.7	561	2	US-09-172-699-20	Sequence 2, Appl1	654	94.5	2.7	1330	3	US-10-124-557-46	Sequence 46, Appl
582	96	2.7	1125	2	US-09-513-783A-152	Sequence 152, Ap	655	94.5	2.7	1330	3	US-10-124-557-60	Sequence 60, Appl
583	96	2.7	1125	2	US-09-430-656-152	Sequence 152, Ap	656	94.5	2.7	1334	2	US-07-757-022B-48	Sequence 48, Appl
584	96	2.7	1125	2	US-10-100-957A-152	Sequence 152, Ap	657	94.5	2.7	1334	3	US-10-124-557-48	Sequence 48, Appl
585	96	2.7	1125	2	US-09-513-783A-22	Sequence 22, Appl	658	94.5	2.7	1361	2	US-07-757-022B-40	Sequence 40, Appl
586	96	2.7	1610	2	US-09-430-656-82	Sequence 22, Appl	659	94.5	2.7	1361	3	US-10-124-557-40	Sequence 40, Appl
587	96	2.7	1610	2	US-10-100-957A-22	Sequence 22, Appl	660	94.5	2.7	1363	2	US-07-757-022B-52	Sequence 52, Appl
588	96	2.7	1939	2	US-10-152-886-43	Sequence 43, Appl	661	94.5	2.7	1363	3	US-10-124-557-52	Sequence 52, Appl
589	96	2.7	5232	2	US-09-248-796A-14121	Sequence 14121, A	662	94.5	2.7	1404	2	US-07-757-022B-2	Sequence 2, Appl1
590	95.5	2.7	561	2	US-10-094-749-2371	Sequence 2371, Ap	663	94.5	2.7	1404	2	US-07-757-022B-62	Sequence 62, Appl1
591	95.5	2.7	739	2	US-09-902-540-10606	Sequence 10606, A	664	94.5	2.7	1404	2	US-09-949-016-10914	Sequence 10914, A
592	95.5	2.7	1287	1	US-08-200-232-2	Sequence 2, Appl1	665	94.5	2.7	1404	2	US-09-298-970A-1	Sequence 1, Appl1
593	95.5	2.7	1287	5	PCT-US95-02219-2	Sequence 2, Appl1	666	94.5	2.7	1404	2	US-09-897-188-1	Sequence 1, Appl1
594	95.5	2.7	1287	5	PCT-US95-02219A-2	Sequence 2, Appl1	667	94.5	2.7	1404	3	US-09-556-246-1	Sequence 1, Appl1
595	95.5	2.7	1568	2	US-09-181-706-2	Sequence 2, Appl1	668	94.5	2.7	1404	3	US-10-124-557-2	Sequence 2, Appl1
596	95.5	2.7	1568	2	US-09-458-791-2	Sequence 2, Appl1	669	94.5	2.7	1404	3	US-10-124-557-62	Sequence 62, Appl
597	95.5	2.7	1568	2	US-09-459-066-2	Sequence 2, Appl1	670	94	2.7	591	2	US-09-949-016-10914	Sequence 10914, A
598	95.5	2.7	1568	2	US-09-459-065-2	Sequence 2, Appl1	671	94	2.7	591	2	US-09-949-016-10915	Sequence 10915, A
599	95.5	2.7	1568	2	US-09-949-016-10643	Sequence 10643, A	672	94	2.7	788	2	US-09-248-796A-20511	Sequence 20511, A
600	95.5	2.7	3118	1	US-08-457-273B-8	Sequence 8, Appl1	673	94	2.7	878	2	US-09-556-706B-2	Sequence 2, Appl1
601	95.5	2.7	178	2	US-09-252-991A-20280	Sequence 20280, A	674	94	2.7	878	2	US-09-538-092-1209	Sequence 2, Appl1
602	95	2.7	584	2	US-09-949-016-7352	Sequence 7352, Ap	675	94	2.7	1080	2	US-09-252-991A-29606	Sequence 29606, A
603	95	2.7	584	2	US-09-252-991A-18292	Sequence 18292, A	676	94	2.7	1287	2	US-09-902-540-10440	Sequence 10440, A
604	95	2.7	643	2	US-09-196-270-3	Sequence 3, Appl1	677	93.5	2.7	365	2	US-09-825-414-50	Sequence 50, Appl1
605	95	2.7	643	2	US-09-487-558B-236	Sequence 236, Ap	678	93.5	2.7	380	2	US-09-050-733-70	Sequence 70, Appl
606	95	2.7	761	2	US-09-902-540-12309	Sequence 12309, A	679	93.5	2.7	666	2	US-09-804-980-70	Sequence 70, Appl
607	95	2.7	917	2	US-09-902-540-15387	Sequence 15387, A	680	93.5	2.7	727	2	US-09-489-039A-14168	Sequence 14168, A
608	95	2.7	937	2	US-09-447-399-4	Sequence 4, Appl1	681	93.5	2.7	809	1	US-08-087-016-2	Sequence 2, Appl1
609	95	2.7	1021	2	US-09-270-767-58808	Sequence 58808, A	682	93.5	2.7	939	2	US-09-489-039A-13915	Sequence 13915, A
610	95	2.7					683	93.5	2.7				

684	93.5	2.7	1876	2	US-09-418-710-71	Sequence 71, Appl	757	92	2.6	423	2	US-09-270-767-40808	Sequence 40808, A
685	93.5	2.7	1876	2	US-09-839-479-70	Sequence 70, Appl	758	92	2.6	423	2	US-09-270-767-56024	Sequence 56024, A
686	93.5	2.7	2179	2	US-09-949-016-8129	Sequence 8129, Ap	759	92	2.6	546	2	US-09-540-236-2574	Sequence 2574, Ap
687	93.5	2.7	3816	2	US-09-428-517-3	Sequence 3, Appl1	760	92	2.6	681	2	US-08-760-615-4	Sequence 4, Appl1
688	93.5	2.7	4572	2	US-10-042-665A-4	Sequence 25477, A	761	92	2.6	681	3	US-09-762-224B-6	Sequence 6, Appl1
689	93	2.7	3222	2	US-09-252-991A-25477	Sequence 4, Appl1	762	92	2.6	724	3	US-09-949-016-10487	Sequence 10487, A
690	93	2.7	380	2	US-09-902-540-10846	Sequence 10846, A	763	92	2.6	726	2	US-09-489-039A-8750	Sequence 8750, Ap
691	93	2.7	414	2	US-09-270-767-11485	Sequence 41485, A	764	92	2.6	780	2	US-09-949-016-10205	Sequence 10205, A
692	93	2.7	486	2	US-10-104-047-3837	Sequence 3837, Ap	765	92	2.6	824	2	US-08-785-310A-7	Sequence 7, Appl1
693	93	2.7	490	2	US-09-109-841-2	Sequence 2, Appl1	766	92	2.6	930	2	US-10-113-794A-1	Sequence 1, Appl1
694	93	2.7	557	2	US-09-248-796A-24387	Sequence 24387, A	767	92	2.6	1187	2	US-09-949-016-6513	Sequence 6513, Ap
695	93	2.7	627	2	US-09-345-473E-47	Sequence 47, Appl	768	92	2.6	1237	1	US-08-241-853-2	Sequence 2, Appl1
696	93	2.7	627	2	US-09-862-027-47	Sequence 47, Appl	769	92	2.6	1237	1	US-08-850-917-2	Sequence 2, Appl1
697	93	2.7	741	2	US-09-248-796A-17282	Sequence 17282, A	770	92	2.6	1381	2	US-09-540-245A-16	Sequence 16, Appl
698	93	2.7	781	2	US-09-248-796A-19137	Sequence 19137, A	771	92	2.6	1381	2	US-10-289-776-16	Sequence 16, Appl
699	93	2.7	824	1	US-08-816-693A-52	Sequence 52, Appl	772	92	2.6	1381	3	US-09-191-651-4	Sequence 4, Appl1
700	93	2.7	824	2	US-08-885-291-52	Sequence 52, Appl	773	92	2.6	1581	2	US-09-110-571-2	Sequence 2, Appl1
701	93	2.7	824	2	US-09-496-672-52	Sequence 52, Appl	774	92	2.6	1687	1	US-08-570-311-29	Sequence 29, Appl
702	93	2.7	907	2	US-08-783-774-2	Sequence 2, Appl1	775	92	2.6	1933	2	US-10-152-886-83	Sequence 83, Appl
703	93	2.7	907	2	US-09-338-599A-1	Sequence 1, Appl1	776	92	2.6	2017	3	US-10-114-270-86	Sequence 86, Appl
704	93	2.7	907	5	PCT-US95-04611A-19	Sequence 19, Appl	777	92	2.6	2169	2	US-09-949-016-69310	Sequence 6930, Ap
705	93	2.7	1018	2	US-10-090-827-6	Sequence 6, Appl1	778	92	2.6	2842	1	US-07-741-940-7	Sequence 7, Appl1
706	93	2.7	1018	2	US-09-397-548-6	Sequence 6, Appl1	779	92	2.6	2842	1	US-08-289-548A-7	Sequence 7, Appl1
707	93	2.7	1036	2	US-10-090-827-7	Sequence 7, Appl1	780	92	2.6	2842	1	US-08-452-654-7	Sequence 7, Appl1
708	93	2.7	1036	2	US-09-397-548-7	Sequence 7, Appl1	781	92	2.6	2842	2	US-08-449-731-7	Sequence 7, Appl1
709	93	2.7	1063	2	US-10-090-827-8	Sequence 8, Appl1	782	92	2.6	2843	1	US-07-741-940-2	Sequence 2, Appl1
710	93	2.7	1063	2	US-09-397-548-8	Sequence 8, Appl1	783	92	2.6	2843	1	US-08-289-548A-2	Sequence 2, Appl1
711	93	2.7	1069	2	US-10-090-827-9	Sequence 9, Appl1	784	92	2.6	2843	1	US-08-452-654-2	Sequence 2, Appl1
712	93	2.7	1091	2	US-10-090-827-5	Sequence 5, Appl1	785	92	2.6	2843	1	US-08-452-655F-2	Sequence 2, Appl1
713	93	2.7	1091	2	US-09-397-548-5	Sequence 5, Appl1	786	92	2.6	2843	1	US-08-452-655B-7	Sequence 7, Appl1
714	93	2.7	1728	2	US-09-949-002-532	Sequence 532, App	787	92	2.6	2843	1	US-08-370-235A-2	Sequence 2, Appl1
715	93	2.7	1821	2	US-09-949-016-5938	Sequence 5938, Ap	788	92	2.6	2843	2	US-08-450-582-2	Sequence 2, Appl1
716	93	2.7	2736	2	US-09-252-991A-30227	Sequence 30227, A	789	92	2.6	2843	2	US-08-449-731-2	Sequence 2, Appl1
717	92.5	2.6	252	1	US-08-460-309-12	Sequence 12, Appl	790	92	2.6	2843	2	US-09-538-092-1007	Sequence 1007, Ap
718	92.5	2.6	252	1	US-08-125-077-12	Sequence 12, Appl	791	92	2.6	2843	6	US-09-442-489F-2	Sequence 2, Appl1
719	92.5	2.6	334	2	US-09-187-970B-7	Sequence 7, Appl1	792	92	2.6	2843	6	US-09-442-489F-7	Sequence 7, Appl1
720	92.5	2.6	380	2	US-09-825-414-40	Sequence 40, Appl	793	92	2.6	2843	6	US-09-821-355A-7	Sequence 7, Appl1
721	92.5	2.6	380	2	US-09-825-414-44	Sequence 44, Appl	794	92	2.6	2973	1	US-09-003-687B-7	Sequence 7, Appl1
722	92.5	2.6	380	2	US-09-825-414-46	Sequence 46, Appl	795	92	2.6	2973	1	US-09-003-687B-7	Sequence 7, Appl1
723	92.5	2.6	380	2	US-09-825-414-52	Sequence 52, Appl	796	92	2.6	2973	2	US-09-136-605-7	Sequence 7, Appl1
724	92.5	2.6	380	2	US-09-248-796A-16546	Sequence 16546, A	797	92	2.6	2973	2	US-09-252-991A-19383	Sequence 19383, A
725	92.5	2.6	525	2	US-09-187-999-9	Sequence 9, Appl1	798	91.5	2.6	352	1	US-08-933-750C-46	Sequence 46, Appl
726	92.5	2.6	535	2	US-09-107-532A-6422	Sequence 6422, Ap	799	91.5	2.6	352	2	US-09-234-613-46	Sequence 27019, A
727	92.5	2.6	569	2	US-09-173-053-18	Sequence 18, Appl	800	91.5	2.6	390	2	US-09-252-991A-27019	Sequence 27227, A
728	92.5	2.6	575	2	US-09-394-142B-20	Sequence 20, Appl	801	91.5	2.6	415	2	US-09-252-991A-27227	Sequence 1888, Ap
729	92.5	2.6	600	2	US-09-248-796A-23971	Sequence 23971, A	802	91.5	2.6	488	2	US-10-094-749-1886	Sequence 1068, Ap
730	92.5	2.6	660	2	US-09-462-606-52	Sequence 52, Appl	803	91.5	2.6	633	2	US-09-710-279-1068	Sequence 1068, Ap
731	92.5	2.6	677	2	US-09-394-142B-6	Sequence 6, Appl1	804	91.5	2.6	685	2	US-09-248-796A-20197	Sequence 20197, A
732	92.5	2.6	756	2	US-10-104-047-2505	Sequence 2505, Ap	805	91.5	2.6	710	2	US-09-171-461-16	Sequence 16, Appl
733	92.5	2.6	784	2	US-09-538-092-1254	Sequence 1254, Ap	806	91.5	2.6	710	2	US-09-970-711-16	Sequence 16, Appl
734	92.5	2.6	786	2	US-09-949-016-10170	Sequence 10170, A	807	91.5	2.6	801	2	US-09-854-856-28	Sequence 28, Appl
735	92.5	2.6	799	2	US-10-094-749-2342	Sequence 2342, Ap	808	91.5	2.6	801	2	US-10-010-720-12	Sequence 12, Appl
736	92.5	2.6	911	2	US-09-902-540-14901	Sequence 14901, A	809	91.5	2.6	829	2	US-09-854-856-12	Sequence 12, Appl
737	92.5	2.6	931	2	US-09-949-016-8987	Sequence 8987, Ap	810	91.5	2.6	829	2	US-10-010-720-12	Sequence 12, Appl
738	92.5	2.6	1297	2	US-09-107-532A-4552	Sequence 4552, Ap	811	91.5	2.6	954	2	US-09-854-856-22	Sequence 22, Appl
739	92.5	2.6	1576	2	US-09-562-702A-24	Sequence 24, Appl	812	91.5	2.6	954	2	US-10-010-720-22	Sequence 22, Appl
740	92.5	2.6	1576	2	US-09-561-818A-24	Sequence 16, Appl	813	91.5	2.6	982	2	US-10-010-720-6	Sequence 6, Appl1
741	92.5	2.6	1576	2	US-10-037-182-16	Sequence 28, Appl	814	91.5	2.6	982	2	US-10-010-720-6	Sequence 6, Appl1
742	92.5	2.6	1584	2	US-09-562-702A-28	Sequence 22, Appl	815	91.5	2.6	1055	1	US-08-659-251-5	Sequence 5, Appl1
743	92.5	2.6	1609	2	US-09-562-702A-22	Sequence 22, Appl	816	91.5	2.6	1055	2	US-09-256-490-5	Sequence 5, Appl1
744	92.5	2.6	1609	2	US-09-561-818A-22	Sequence 22, Appl	817	91.5	2.6	1055	5	PCT-US96-11445-5	Sequence 5, Appl1
745	92.5	2.6	1609	2	US-10-037-182-14	Sequence 14, Appl	818	91.5	2.6	1074	2	US-09-252-991A-21193	Sequence 21193, A
746	92.5	2.6	1617	2	US-09-562-702A-26	Sequence 26, Appl	819	91.5	2.6	1140	2	US-09-538-092-647	Sequence 647, Ap
747	92.5	2.6	1824	2	US-09-543-681A-5009	Sequence 5009, Ap	820	91.5	2.6	1168	2	US-09-661-322A-22	Sequence 22, Appl
748	92.5	2.6	1966	1	US-08-804-327C-9	Sequence 9, Appl1	821	91.5	2.6	1330	2	US-10-164-595-58	Sequence 58, Appl
749	92.5	2.6	1996	1	US-08-804-198-3	Sequence 3, Appl1	822	91.5	2.6	1404	2	US-10-164-595-10827	Sequence 10827, A
750	92.5	2.6	2753	2	US-09-949-016-7659	Sequence 7659, Ap	823	91.5	2.6	1411	2	US-09-849-016-10627	Sequence 26, Appl
751	92.5	2.6	2753	2	US-09-949-016-7660	Sequence 7660, Ap	824	91.5	2.6	2064	2	US-09-854-856-26	Sequence 26, Appl
752	92.5	2.6	3852	2	US-10-025-225-4	Sequence 4, Appl1	825	91.5	2.6	2064	2	US-10-010-720-26	Sequence 10, Appl
753	92.5	2.6	3924	2	US-09-538-092-1246	Sequence 1246, Ap	826	91.5	2.6	2092	2	US-09-854-856-10	Sequence 10, Appl
754	92.5	2.6	4585	2	US-10-025-225-6	Sequence 6, Appl1	827	91.5	2.6	2202	2	US-10-010-720-10	Sequence 10, Appl
755	92.5	2.6	4585	2	US-10-025-225-8	Sequence 8, Appl1	828	91.5	2.6	2202	2	US-09-854-856-24	Sequence 24, Appl
756	92.5	2.6	4589	2	US-10-025-225-2	Sequence 2, Appl1	829	91.5	2.6	2201	2	US-10-010-720-24	Sequence 24, Appl

830	91.5	2.6	2229	2	US-09-854-856-8	Sequence 8, Appli	903	90	2.6	366	2	US-09-176-657-2	Sequence 2, Appli
831	91.5	2.6	2229	2	US-10-010-720-8	Sequence 8, Appli	904	90	2.6	366	2	US-09-421-299-2	Sequence 2, Appli
832	91.5	2.6	2843	2	US-10-092-138A-30	Sequence 30, Appli	905	90	2.6	389	2	US-09-134-001C-3161	Sequence 3161, Ap
833	91.5	2.6	2843	2	US-08-681-219A-30	Sequence 30, Appli	906	90	2.6	391	2	US-09-248-796A-14619	Sequence 14619, A
834	91	2.6	77	2	US-09-513-999C-6277	Sequence 6277, Ap	907	90	2.6	428	2	US-09-538-092-531	Sequence 531, App
835	91	2.6	148	2	US-09-252-991A-29694	Sequence 29694, A	908	90	2.6	431	2	US-09-949-016-8253	Sequence 8253, App
836	91	2.6	337	2	US-08-930-830B-2	Sequence 2, Appli	909	90	2.6	439	2	US-09-134-000C-6557	Sequence 6557, Ap
837	91	2.6	344	2	US-09-771-161A-173	Sequence 173, App	910	90	2.6	494	2	US-09-252-991A-28022	Sequence 28022, A
838	91	2.6	379	2	US-09-252-991A-28086	Sequence 28086, A	911	90	2.6	514	2	US-09-583-110-5001	Sequence 5001, Ap
839	91	2.6	454	2	US-09-270-767-45646	Sequence 45646, A	912	90	2.6	539	2	US-09-107-413-2719	Sequence 2719, Ap
840	91	2.6	481	2	US-09-949-016-9581	Sequence 9581, Ap	913	90	2.6	610	2	US-09-538-092-1378	Sequence 1378, Ap
841	91	2.6	564	2	US-09-809-665A-30	Sequence 30, Appli	914	90	2.6	820	2	US-09-248-796A-17231	Sequence 17231, A
842	91	2.6	602	2	US-10-094-749-2246	Sequence 2246, Ap	915	90	2.6	965	2	US-09-993-777-6	Sequence 6, Appli
843	91	2.6	608	2	US-09-949-016-11148	Sequence 11148, A	916	90	2.6	985	2	US-09-993-777-6	Sequence 66, Appli
844	91	2.6	608	2	US-09-949-016-11149	Sequence 11149, A	917	90	2.6	985	2	US-09-994-064-6	Sequence 6, Appli
845	91	2.6	608	2	US-09-949-016-11150	Sequence 11150, A	918	90	2.6	985	2	US-09-994-064-6	Sequence 66, Appli
846	91	2.6	608	2	US-09-949-016-11151	Sequence 11151, A	919	90	2.6	985	5	PCT-US96-03916-66	Sequence 66, Appli
847	91	2.6	626	2	US-09-345-473E-43	Sequence 43, Appli	920	90	2.6	985	5	PCT-US96-03916-66	Sequence 66, Appli
848	91	2.6	626	2	US-09-862-027-43	Sequence 43, Appli	921	90	2.6	1154	2	US-09-457-708-2	Sequence 2, Appli
849	91	2.6	646	2	US-09-252-991A-26479	Sequence 26479, A	922	90	2.6	1154	2	US-09-457-708-2	Sequence 2, Appli
850	91	2.6	712	1	US-08-587-889-2	Sequence 2, Appli	923	90	2.6	1163	2	US-09-976-594-989	Sequence 989, App
851	91	2.6	712	1	US-08-980-060-5	Sequence 5, Appli	924	90	2.6	1183	2	US-09-134-001C-3530	Sequence 3530, Ap
852	91	2.6	712	2	US-09-307-185-5	Sequence 5, Appli	925	90	2.6	1239	2	US-09-344-624-4	Sequence 4, Appli
853	91	2.6	712	2	US-09-773-753-5	Sequence 5, Appli	926	90	2.6	1254	2	US-10-375-693-30	Sequence 30, Appli
854	91	2.6	712	2	US-09-771-161A-262	Sequence 262, App	927	90	2.6	1308	2	US-09-134-000C-6588	Sequence 6588, Ap
855	91	2.6	712	2	US-09-771-161A-263	Sequence 263, App	928	90	2.6	1704	2	US-08-485-3558-40	Sequence 40, Appli
856	91	2.6	712	2	US-09-771-161A-264	Sequence 264, App	929	90	2.6	1706	2	US-09-066-330-10	Sequence 10, Appli
857	91	2.6	712	5	PCT-US96-09193-2	Sequence 2, Appli	930	90	2.6	1837	2	US-08-928-361B-5	Sequence 5, Appli
858	91	2.6	759	2	US-10-104-047-3770	Sequence 2770, Ap	931	90	2.6	1837	2	US-09-508-995A-5	Sequence 5, Appli
859	91	2.6	1028	2	US-09-939-853A-17	Sequence 17, Appli	932	90	2.6	2446	2	US-09-949-016-11439	Sequence 11439, A
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863	91	2.6	1226	5	US-09-949-002-313	Sequence 313, App	936	90	2.6	532	2	US-09-538-092-1096	Sequence 1096, Ap
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867	91	2.6	1350	2	US-09-581-472B-2	Sequence 2, Appli	940	90	2.6	660	2	US-08-819-177-1	Sequence 1, Appli
868	91	2.6	1792	2	US-09-561-818A-12	Sequence 12, Appli	941	90	2.6	664	1	US-08-852-153-8	Sequence 9759, Ap
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870	91	2.6	2090	2	US-09-538-092-1081	Sequence 1081, Ap	943	90	2.6	675	2	US-09-332-063-2	Sequence 2, Appli
871	91	2.6	2120	2	US-09-949-016-9768	Sequence 38, Appli	944	90	2.6	675	2	US-09-332-063-3	Sequence 3, Appli
872	90.5	2.6	252	1	US-08-152-019A-38	Sequence 12, Appli	945	90	2.6	741	2	US-09-854-856-60	Sequence 60, Appli
873	90.5	2.6	357	5	US-08-145-006C-12	Sequence 12, Appli	946	90	2.6	759	2	US-10-010-720-60	Sequence 60, Appli
874	90.5	2.6	357	5	PCT-US94-00545-12	Sequence 12, Appli	947	90	2.6	759	2	US-09-337-387-12	Sequence 12, Appli
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876	90.5	2.6	368	2	US-09-107-433-2767	Sequence 2767, Ap	949	90	2.6	759	2	US-09-854-856-44	Sequence 44, Appli
877	90.5	2.6	415	2	US-09-902-540-11959	Sequence 11959, A	950	90	2.6	769	2	US-10-010-720A-44	Sequence 44, Appli
878	90.5	2.6	694	2	US-09-949-016-7117	Sequence 7, Appli	951	90	2.6	824	2	US-09-949-002-448	Sequence 448, App
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880	90.5	2.6	897	2	US-09-866-020A-2	Sequence 2, Appli	953	90	2.6	837	2	US-09-634-286A-2	Sequence 2, Appli
881	90.5	2.6	906	2	US-08-630-916A-48	Sequence 48, Appli	954	90	2.6	837	2	US-10-247-685-2	Sequence 2, Appli
882	90.5	2.6	908	1	US-08-249-380-2	Sequence 2, Appli	955	90	2.6	837	2	US-09-949-002-380	Sequence 380, App
883	90.5	2.6	910	2	US-09-270-767-42083	Sequence 42083, A	956	90	2.6	837	2	US-10-012-231A-317	Sequence 317, App
884	90.5	2.6	923	2	US-09-825-147-2	Sequence 2, Appli	957	90	2.6	837	2	US-10-015-389A-317	Sequence 317, App
885	90.5	2.6	923	2	US-09-813-148-2	Sequence 2, Appli	958	90	2.6	837	2	US-10-006-768A-317	Sequence 317, App
886	90.5	2.6	1058	2	US-09-538-092-985	Sequence 985, App	959	90	2.6	837	2	US-10-015-392A-317	Sequence 317, App
887	90.5	2.6	1083	2	US-09-538-092-812	Sequence 812, App	960	90	2.6	837	2	US-10-015-671A-317	Sequence 317, App
888	90.5	2.6	1168	1	US-08-448-170-6	Sequence 6, Appli	961	90	2.6	837	2	US-10-015-393A-317	Sequence 317, App
889	90.5	2.6	1168	2	US-08-961-803-8	Sequence 8, Appli	962	90	2.6	837	2	US-10-011-833A-317	Sequence 317, App
890	90.5	2.6	1388	2	US-09-270-767-44387	Sequence 44387, A	963	90	2.6	837	2	US-10-006-041A-317	Sequence 317, App
891	90.5	2.6	1609	2	US-09-538-092-900	Sequence 900, App	964	90	2.6	837	2	US-10-012-064A-317	Sequence 317, App
892	90.5	2.6	2004	2	US-09-854-856-58	Sequence 58, Appli	965	90	2.6	837	3	US-10-015-392A-317	Sequence 317, App
893	90.5	2.6	2004	2	US-10-010-720-58	Sequence 58, Appli	966	90	2.6	837	3	US-10-011-795B-317	Sequence 317, App
894	90.5	2.6	2032	2	US-09-854-856-42	Sequence 42, Appli	967	90	2.6	837	3	US-10-015-386A-317	Sequence 317, App
895	90.5	2.6	2032	2	US-10-010-720-42	Sequence 42, Appli	968	90	2.6	837	3	US-10-012-121A-317	Sequence 317, App
896	90.5	2.6	2141	2	US-09-854-856-56	Sequence 56, Appli	969	90	2.6	837	3	US-10-006-485A-317	Sequence 317, App
897	90.5	2.6	2141	2	US-10-010-720-56	Sequence 56, Appli	970	90	2.6	837	3	US-10-006-746A-317	Sequence 317, App
898	90.5	2.6	2169	2	*US-09-854-856-40	Sequence 40, Appli	971	90	2.6	837	3	US-10-012-752A-317	Sequence 317, App
899	90.5	2.6	2169	2	US-10-010-720-40	Sequence 40, Appli	972	90	2.6	837	3	US-10-017-253A-317	Sequence 317, App
900	90.5	2.6	6095	2	US-09-144-085-2	Sequence 2, Appli	973	90	2.6	837	3	US-10-015-519A-317	Sequence 317, App
901	90	2.6	208	2	US-10-104-047-2284	Sequence 2284, A	974	90	2.6	837	3	US-10-015-715A-317	Sequence 317, App
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977	89.5	2.6	870	2	US-09-538-092-77	Sequence 77, Appl	1050	88.5	2.5	660	2	US-09-724-475-2	Sequence 2, Appl1
978	89.5	2.6	894	2	US-09-854-856-54	Sequence 54, Appl	1051	88.5	2.5	660	5	PCT-US93-08849A-2	Sequence 2, Appl1
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980	89.5	2.6	901	2	US-09-828-062-8	Sequence 8, Appl1	1053	88.5	2.5	819	2	US-09-976-594-369	Sequence 369, App
981	89.5	2.6	922	2	US-09-854-856-38	Sequence 38, Appl1	1054	88.5	2.5	827	2	US-09-949-016-7807	Sequence 7807, Ap
982	89.5	2.6	922	2	US-09-198-452A-15	Sequence 15, Appl	1055	88.5	2.5	839	2	US-09-107-532A-6629	Sequence 6829, Ap
983	89.5	2.6	922	2	US-10-010-720-38	Sequence 38, Appl	1056	88.5	2.5	910	2	US-08-997-685A-2	Sequence 2, Appl1
984	89.5	2.6	1058	1	US-08-247-904B-14	Sequence 14, Appl	1057	88.5	2.5	910	2	US-09-086-436-31	Sequence 31, Appl
985	89.5	2.6	1058	1	US-08-767-942A-15	Sequence 15, Appl	1058	88.5	2.5	977	2	US-09-248-796A-15579	Sequence 15579, A
986	89.5	2.6	1215	2	US-09-949-002-321	Sequence 321, App	1059	88.5	2.5	1068	1	US-08-396-479B-12	Sequence 12, Appl
987	89.5	2.6	1298	1	US-08-690-473-2	Sequence 2, Appl1	1060	88.5	2.5	1068	1	US-08-818-823-12	Sequence 12, Appl
988	89.5	2.6	1298	2	US-09-259-821A-2	Sequence 2, Appl1	1061	88.5	2.5	1078	1	US-09-949-016-9573	Sequence 9573, Ap
989	89.5	2.6	1298	2	US-08-843-659-2	Sequence 2, Appl1	1062	88.5	2.5	1351	2	US-09-489-039A-11032	Sequence 11032, A
990	89.5	2.6	1298	2	US-09-825-288A-2	Sequence 2, Appl1	1063	88.5	2.5	1475	2	US-09-538-092-1160	Sequence 1160, Ap
991	89.5	2.6	1463	2	US-09-445-353E-3	Sequence 3, Appl1	1064	88.5	2.5	5087	2	US-09-144-085-1	Sequence 1, Appl1
992	89.5	2.6	1734	2	US-09-862-027-81	Sequence 81, Appl	1065	88.5	2.5	5179	2	US-09-338-092-1258	Sequence 1258, Ap
993	89.5	2.6	1769	2	US-09-949-016-8280	Sequence 8280, Ap	1066	88	2.5	182	2	US-09-252-991A-20676	Sequence 20676, A
994	89.5	2.6	1769	2	US-09-949-016-8281	Sequence 8281, Ap	1067	88	2.5	183	7	US-09-248-796A-19222	Patent No. 5168049
995	89.5	2.6	1769	2	US-09-949-016-8282	Sequence 8282, Ap	1068	88	2.5	194	2	US-09-248-796A-19222	Sequence 19222, A
996	89.5	2.6	1803	2	US-09-902-540-15978	Sequence 15978, A	1069	88	2.5	229	2	US-09-252-991A-23807	Sequence 23807, A
997	89.5	2.6	1813	2	US-09-949-016-8283	Sequence 8283, Ap	1070	88	2.5	233	2	US-09-252-991A-21274	Sequence 21274, A
998	89.5	2.6	1813	2	US-09-949-016-8284	Sequence 8284, Ap	1071	88	2.5	337	2	US-09-248-796A-19866	Sequence 19866, A
999	89.5	2.6	1813	2	US-09-949-016-8285	Sequence 8285, Ap	1072	88	2.5	374	2	US-09-710-279-1664	Sequence 1664, Ap
1000	89.5	2.6	2137	2	US-09-134-001C-4463	Sequence 4463, Ap	1073	88	2.5	442	2	US-09-489-039A-11770	Sequence 11770, A
1001	89.5	2.6	2680	2	US-09-489-039A-7973	Sequence 7973, Ap	1074	88	2.5	468	2	US-08-561-083-10	Sequence 10, Appl
1002	89.5	2.6	2870	2	US-09-479-467A-15	Sequence 15, Appl	1075	88	2.5	468	2	US-09-536-784-10	Sequence 10, Appl
1003	89.5	2.6	2870	2	US-09-655-160-15	Sequence 15, Appl	1076	88	2.5	468	2	US-09-765-271-10	Sequence 10, Appl
1004	89.5	2.6	3178	2	US-09-479-467A-4	Sequence 4, Appl1	1077	88	2.5	468	2	US-09-765-272A-10	Sequence 10, Appl
1005	89.5	2.6	3178	2	US-09-655-160-4	Sequence 4, Appl1	1078	88	2.5	477	2	US-09-248-796A-20759	Sequence 20759, A
1006	89	2.5	322	2	US-09-248-796A-17229	Sequence 17229, A	1079	88	2.5	500	2	US-10-104-047-2718	Sequence 2718, Ap
1007	89	2.5	343	1	US-08-599-171A-28	Sequence 28, Appl	1080	88	2.5	530	2	US-09-971-773-73	Sequence 73, Appl
1008	89	2.5	343	1	US-08-646-590B-28	Sequence 28, Appl	1081	88	2.5	627	2	US-09-071-035-218	Sequence 218, App
1009	89	2.5	343	1	US-09-069-226-28	Sequence 28, Appl	1082	88	2.5	627	2	US-10-206-576-218	Sequence 218, App
1010	89	2.5	343	2	US-09-412-184-38	Sequence 28, Appl	1083	88	2.5	634	2	US-09-602-777A-272	Sequence 272, App
1011	89	2.5	484	2	US-09-605-703B-2414	Sequence 2414, Ap	1084	88	2.5	634	2	US-09-252-991A-13154	Sequence 19154, A
1012	89	2.5	681	2	US-09-336-910A-2	Sequence 2, Appl1	1085	88	2.5	639	2	US-09-134-000A-6124	Sequence 6124, Ap
1013	89	2.5	866	2	US-09-079-415-6	Sequence 6, Appl1	1086	88	2.5	717	2	US-09-443-681A-5706	Sequence 5706, Ap
1014	89	2.5	866	2	US-08-750-458A-2	Sequence 2, Appl1	1087	88	2.5	805	2	US-09-425-335-6	Sequence 35, Appl
1015	89	2.5	1154	2	US-09-134-000C-6122	Sequence 6122, App	1088	88	2.5	830	2	US-09-562-737-35	Sequence 8, Appl1
1016	89	2.5	1164	2	US-09-538-092-399	Sequence 399, App	1089	88	2.5	1065	1	US-08-400-159-8	Sequence 48, Appl
1017	89	2.5	1225	2	US-09-501-171-4	Sequence 4, Appl1	1090	88	2.5	1098	2	US-09-602-787A-48	Sequence 2, Appl1
1018	89	2.5	1225	2	US-09-949-016-6063	Sequence 6063, Ap	1091	88	2.5	1402	2	US-09-513-878A-2	Sequence 1044, Ap
1019	89	2.5	1245	2	US-10-172-502-19	Sequence 19, Appl	1092	88	2.5	1427	2	US-09-538-092-1044	Sequence 46, Appl
1020	89	2.5	1257	1	US-08-340-428B-49	Sequence 49, Appl	1093	88	2.5	1874	2	US-09-602-787A-46	Sequence 12, Appl
1021	89	2.5	145	2	US-09-252-991A-31281	Sequence 31281, A	1094	88	2.5	2466	2	US-09-080-855-12	Sequence 12, Appl
1022	88.5	2.5	207	1	US-08-177-109A-59	Sequence 59, Appl	1095	88	2.5	2466	5	US-09-566-076-12	Sequence 12, Appl
1023	88.5	2.5	268	1	US-08-687-706-59	Sequence 59, Appl	1096	88	2.5	2466	5	PCT-US94-0994-2	Sequence 2, Appl1
1024	88.5	2.5	268	2	US-09-902-540-13592	Sequence 13592, A	1097	88	2.5	3633	2	US-09-341-461-2	Sequence 1769, A
1025	88.5	2.5	354	2	US-10-104-047-3151	Sequence 3151, Ap	1098	87.5	2.5	281	2	US-09-248-796A-17769	Sequence 18944, A
1026	88.5	2.5	357	1	US-08-078-683A-8	Sequence 8, Appl1	1099	87.5	2.5	315	2	US-09-248-796A-16944	Sequence 5, Appl1
1027	88.5	2.5	357	2	US-08-471-970A-8	Sequence 8, Appl1	1100	87.5	2.5	342	2	US-09-930-830B-5	Sequence 197, App
1028	88.5	2.5	357	2	US-09-723-677B-8	Sequence 8, Appl1	1101	87.5	2.5	346	2	US-09-991-181-197	Sequence 197, App
1029	88.5	2.5	380	2	US-09-825-414-42	Sequence 42, Appl	1102	87.5	2.5	346	2	US-09-990-444-197	Sequence 197, App
1030	88.5	2.5	380	2	US-09-825-414-48	Sequence 48, Appl	1103	87.5	2.5	346	2	US-09-997-333-197	Sequence 197, App
1031	88.5	2.5	397	2	US-08-991-426-4	Sequence 4, Appl1	1104	87.5	2.5	346	2	US-09-992-598-197	Sequence 197, App
1032	88.5	2.5	397	2	US-09-143-470-4	Sequence 4, Appl1	1105	87.5	2.5	346	2	US-09-989-735-197	Sequence 197, App
1033	88.5	2.5	397	2	US-08-649-006A-4	Sequence 4, Appl1	1106	87.5	2.5	346	2	US-09-833-041A-77	Sequence 77, Appl
1034	88.5	2.5	397	2	US-09-771-023-4	Sequence 4, Appl1	1107	87.5	2.5	346	3	US-09-989-726-197	Sequence 197, App
1035	88.5	2.5	404	2	US-09-328-352-6480	Sequence 6480, Ap	1108	87.5	2.5	346	3	US-09-997-514-197	Sequence 197, App
1036	88.5	2.5	481	2	US-09-248-796A-15894	Sequence 15894, A	1109	87.5	2.5	346	3	US-09-989-728-197	Sequence 197, App
1037	88.5	2.5	512	2	US-09-390-234-24	Sequence 24, Appl	1110	87.5	2.5	346	3	US-09-997-349-197	Sequence 197, App
1038	88.5	2.5	512	2	US-09-603-311-24	Sequence 24, Appl	1111	87.5	2.5	346	3	US-09-997-653-197	Sequence 197, App
1039	88.5	2.5	512	2	US-09-570-856B-30	Sequence 30, Appl	1112	87.5	2.5	346	3	US-09-989-293A-197	Sequence 197, App
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1041	88.5	2.5	530	2	US-09-222-817-14	Sequence 14, Appl	1114	87.5	2.5	404	2	US-10-029-180-78	Sequence 78, Appl
1042	88.5	2.5	530	2	US-09-222-786-12	Sequence 12, Appl	1115	87.5	2.5	444	2	US-10-029-180-112	Sequence 112, App
1043	88.5	2.5	530	2	US-09-222-786-14	Sequence 14, Appl	1116	87.5	2.5	444	2	US-09-902-540-16488	Sequence 16488, A
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1047	88.5	2.5	660	2	US-09-402-776-2	Sequence 2, Appl1	1120	87.5	2.5	556	2	US-09-487-558B-476	Sequence 426, App
1048	88.5	2.5	660	2	US-08-470-246-2	Sequence 2, Appl1	1121	87.5	2.5	558	2	US-09-902-540-16460	Sequence 16460, A

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1123	87.5	2.5	636	2	US-09-538-092-910	Sequence 910, App	1196	87	2.5	1265	2	US-09-071-035-118	Sequence 418, App
1124	87.5	2.5	647	2	US-10-094-749-3043	Sequence 3043, App	1197	87	2.5	1265	2	US-10-206-576-418	Sequence 418, App
1125	87.5	2.5	649	2	US-09-902-540-10443	Sequence 10443, A	1198	87	2.5	1278	2	US-09-134-000C-6043	Sequence 6043, App
1126	87.5	2.5	677	1	US-08-522-269B-3	Sequence 3, App1	1199	87	2.5	1461	1	US-10-094-749-2733	Sequence 2733, App
1127	87.5	2.5	677	2	US-09-294-923-3	Sequence 3, App1	1200	87	2.5	1461	1	US-08-790-912-4	Sequence 4, App1
1128	87.5	2.5	773	1	US-08-484-101B-42	Sequence 42, App1	1201	87	2.5	2254	2	US-09-949-016-9270	Sequence 9270, App
1129	87.5	2.5	773	1	US-08-484-101B-44	Sequence 42, App1	1202	87	2.5	2254	2	US-09-051-019-2	Sequence 2, App1
1130	87.5	2.5	773	2	US-08-714-524D-42	Sequence 42, App1	1203	87	2.5	2453	2	US-09-632-03B-4	Sequence 4, App1
1131	87.5	2.5	773	2	US-08-714-524D-44	Sequence 44, App1	1204	87	2.5	2595	2	US-09-036-987A-2	Sequence 2, App1
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1133	87.5	2.5	777	2	US-09-949-016-8707	Sequence 8707, App	1206	87	2.5	2595	2	US-09-603-207-2	Sequence 2, App1
1134	87.5	2.5	870	1	US-08-266-311-1	Sequence 1, App1	1207	87	2.5	2595	3	US-10-329-148A-2	Sequence 2, App1
1135	87.5	2.5	870	2	US-08-467-527A-1	Sequence 1, App1	1208	87	2.5	3256	2	US-09-919-172-98	Sequence 98, App1
1136	87.5	2.5	870	2	US-08-467-528-1	Sequence 1, App1	1209	87	2.5	3256	2	US-09-976-594-22	Sequence 22, App1
1137	87.5	2.5	1013	2	US-09-612-402B-15	Sequence 15, App1	1210	87	2.5	3256	2	US-09-919-039-21	Sequence 21, App1
1138	87.5	2.5	1013	2	US-09-542-520-15	Sequence 15, App1	1211	86.5	2.5	253	2	US-09-252-991A-31638	Sequence 31638, A
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1140	87.5	2.5	1501	1	US-08-716-679-3	Sequence 3, App1	1213	86.5	2.5	258	2	US-10-015-389A-153	Sequence 153, App
1141	87.5	2.5	4150	2	US-09-428-517-2	Sequence 2, App1	1214	86.5	2.5	258	2	US-10-006-768A-153	Sequence 153, App
1142	87.5	2.5	166	2	US-09-252-991A-20684	Sequence 20684, A	1215	86.5	2.5	258	2	US-10-015-671A-153	Sequence 153, App
1143	87	2.5	166	2	US-09-270-767-60635	Sequence 60635, A	1216	86.5	2.5	258	2	US-10-015-393A-153	Sequence 153, App
1144	87	2.5	255	2	US-09-107-532A-5821	Sequence 5821, App	1217	86.5	2.5	258	2	US-10-011-833A-153	Sequence 153, App
1145	87	2.5	336	2	US-09-583-110-3857	Sequence 3957, App	1218	86.5	2.5	258	2	US-10-006-041A-153	Sequence 153, App
1146	87	2.5	337	2	US-09-107-433-2997	Sequence 2997, App	1219	86.5	2.5	258	2	US-10-012-064A-153	Sequence 153, App
1147	87	2.5	356	2	US-09-270-767-45036	Sequence 45036, A	1220	86.5	2.5	258	2	US-10-015-392A-153	Sequence 153, App
1148	87	2.5	431	2	US-09-270-767-45143	Sequence 45143, A	1221	86.5	2.5	258	3	US-10-011-795B-153	Sequence 153, App
1149	87	2.5	463	1	US-08-853-659A-52	Sequence 52, App1	1222	86.5	2.5	258	3	US-10-015-386A-153	Sequence 153, App
1150	87	2.5	469	2	US-09-252-991A-30596	Sequence 30596, A	1223	86.5	2.5	258	3	US-10-012-121A-153	Sequence 153, App
1151	87	2.5	496	2	US-09-543-681A-7087	Sequence 7087, App	1224	86.5	2.5	258	3	US-10-006-485A-153	Sequence 153, App
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1153	87	2.5	534	1	US-09-270-117-1	Sequence 1, App1	1226	86.5	2.5	258	3	US-10-012-752A-153	Sequence 153, App
1154	87	2.5	534	2	US-09-046-572-1	Sequence 1, App1	1227	86.5	2.5	258	3	US-10-017-253A-153	Sequence 153, App
1155	87	2.5	539	2	US-09-252-991A-24784	Sequence 24784, A	1228	86.5	2.5	258	3	US-10-015-519A-153	Sequence 153, App
1156	87	2.5	554	2	US-09-948-016-7429	Sequence 7429, App	1229	86.5	2.5	258	3	US-10-015-715A-153	Sequence 153, App
1157	87	2.5	583	2	US-09-328-352-6422	Sequence 6422, App	1230	86.5	2.5	258	3	US-10-007-236A-153	Sequence 153, App
1158	87	2.5	598	2	US-09-866-028-69	Sequence 69, App1	1231	86.5	2.5	261	2	US-09-198-452A-559	Sequence 559, App
1159	87	2.5	598	2	US-09-944-584-69	Sequence 69, App1	1232	86.5	2.5	268	2	US-09-438-185A-521	Sequence 521, App
1160	87	2.5	598	2	US-09-945-584-69	Sequence 69, App1	1233	86.5	2.5	358	1	US-08-034-650-10	Sequence 10, App1
1161	87	2.5	598	2	US-09-944-944-69	Sequence 69, App1	1234	86.5	2.5	358	1	US-08-449-015-10	Sequence 10, App1
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1163	87	2.5	598	3	US-09-944-884-69	Sequence 69, App1	1236	86.5	2.5	362	2	US-09-126-121-3	Sequence 3, App1
1164	87	2.5	605	1	US-08-687-956A-1	Sequence 1, App1	1237	86.5	2.5	362	2	US-09-107-979-3	Sequence 3, App1
1165	87	2.5	660	2	US-08-542-634-14	Sequence 14, App1	1238	86.5	2.5	426	2	US-09-107-532A-7172	Sequence 7172, App
1166	87	2.5	660	5	PCR-US95-13703-14	Sequence 14, App1	1239	86.5	2.5	515	2	US-09-487-558B-384	Sequence 384, App
1167	87	2.5	673	2	US-09-063-950-2	Sequence 2, App1	1240	86.5	2.5	557	2	US-08-962-281-4	Sequence 4, App1
1168	87	2.5	673	2	US-09-991-181-52	Sequence 52, App1	1241	86.5	2.5	573	2	US-09-902-540-12155	Sequence 12155, A
1169	87	2.5	673	2	US-09-990-444-52	Sequence 52, App1	1242	86.5	2.5	713	2	US-08-899-437-2	Sequence 2, App1
1170	87	2.5	673	2	US-09-997-333-52	Sequence 52, App1	1243	86.5	2.5	713	2	US-09-126-121-2	Sequence 2, App1
1171	87	2.5	673	2	US-09-992-598-52	Sequence 52, App1	1244	86.5	2.5	713	2	US-09-107-979-2	Sequence 2, App1
1172	87	2.5	673	3	US-09-989-735-52	Sequence 52, App1	1245	86.5	2.5	751	2	US-08-946-026-6	Sequence 6, App1
1173	87	2.5	673	3	US-09-989-726-52	Sequence 52, App1	1246	86.5	2.5	846	1	US-09-252-991A-18035	Sequence 18035, A
1174	87	2.5	673	3	US-09-997-514-52	Sequence 52, App1	1247	86.5	2.5	846	1	US-07-731-157A-5	Sequence 5, App1
1175	87	2.5	673	3	US-09-989-728-52	Sequence 52, App1	1248	86.5	2.5	846	1	US-08-541-780-5	Sequence 5, App1
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1177	87	2.5	673	3	US-09-997-653-52	Sequence 52, App1	1250	86.5	2.5	862	1	US-08-325-267A-4	Sequence 4, App1
1178	87	2.5	673	3	US-09-989-293A-52	Sequence 52, App1	1251	86.5	2.5	894	2	US-08-362-525-22	Sequence 22, App1
1179	87	2.5	685	2	US-10-104-047-2916	Sequence 2916, App	1252	86.5	2.5	894	2	US-08-971-692-15	Sequence 15, App1
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1182	87	2.5	712	2	US-09-248-796A-14274	Sequence 14274, A	1255	86.5	2.5	907	2	US-09-020-222-26	Sequence 26, App1
1183	87	2.5	713	2	US-09-489-039A-14274	Sequence 9317, App	1256	86.5	2.5	907	2	US-09-068-377-26	Sequence 26, App1
1184	87	2.5	722	2	US-09-902-540-10649	Sequence 10649, A	1257	86.5	2.5	1001	2	US-10-104-047-2283	Sequence 2283, App
1185	87	2.5	741	2	US-09-949-016-11524	Sequence 11523, A	1258	86.5	2.5	1045	2	US-10-104-047-2830	Sequence 2830, App
1186	87	2.5	741	2	US-09-949-016-11524	Sequence 11523, A	1259	86.5	2.5	1123	2	US-09-408-865-1	Sequence 1, App1
1187	87	2.5	800	2	US-09-252-991A-20437	Sequence 20437, A	1260	86.5	2.5	1537	1	US-08-325-267A-2	Sequence 2, App1
1188	87	2.5	802	2	US-09-134-001C-3840	Sequence 3840, App	1261	86.5	2.5	1537	3	US-09-487-558B-104	Sequence 104, App
1189	87	2.5	859	2	US-09-902-540-14220	Sequence 14220, A	1262	86.5	2.5	1537	3	US-10-324-035-17	Sequence 17, App1
1190	87	2.5	1001	2	US-10-415-147-3	Sequence 3, App1	1263	86.5	2.5	1919	2	US-10-152-886-13	Sequence 13, App1
1191	87	2.5	1004	2	US-09-268-347-30	Sequence 30, App1	1264	86.5	2.5	2756	1	US-08-375-709-11	Sequence 11, App1
1192	87	2.5	1118	2	US-09-252-991A-32439	Sequence 32439, A	1265	86.5	2.5	2756	1	US-08-752-929-11	Sequence 11, App1
1193	87	2.5	1135	2	US-08-981-998A-5	Sequence 5, App1	1266	86.5	2.5	2756	2	US-09-090-793-7	Sequence 7, App1
1194	87	2.5	1231	2	US-09-071-035-420	Sequence 420, App1	1267	86.5	2.5	2756	2	US-09-231-899-7	Sequence 7, App1

1268	86.5	2.5	3730	2	US-09-949-016-9908	Sequence 9908, Ap	1341	85	2.4	503	2	US-09-252-991A-27888	Sequence 27888, A
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1270	86.5	2.5	3969	2	US-09-538-092-1262	Sequence 1262, Ap	1343	85	2.4	520	5	PCT-US91-08177-11	Sequence 11, Appl1
1271	86.5	2.5	4654	2	US-08-476-515A-84	Sequence 84, Appl	1344	85	2.4	572	2	US-09-270-767-59816	Sequence 59816, A
1272	86.5	2.5	4655	2	US-08-652-877-84	Sequence 84, Appl	1345	85	2.4	606	2	US-09-252-991A-130814	Sequence 130814, A
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1274	86.5	2.5	4655	2	US-08-652-877-88	Sequence 88, Appl	1347	85	2.4	610	1	US-08-119-2628-6	Sequence 11, Appl
1275	86.5	2.5	4655	2	US-08-652-877-90	Sequence 90, Appl	1348	85	2.4	610	1	US-08-135-929A-11	Sequence 11, Appl
1276	86	2.5	290	2	US-09-252-991A-22797	Sequence 22797, A	1349	85	2.4	610	1	US-08-234-265A-11	Sequence 11, Appl
1277	86	2.5	489	2	US-10-104-047-3922	Sequence 2922, Ap	1350	85	2.4	634	2	US-09-949-016-11734	Sequence 11734, A
1278	86	2.5	505	2	US-09-270-767-44797	Sequence 44797, A	1351	85	2.4	650	2	US-09-248-796A-18020	Sequence 18020, A
1279	86	2.5	559	2	US-09-540-226-3631	Sequence 3631, Ap	1352	85	2.4	650	2	US-09-489-039A-19100	Sequence 12100, A
1280	86	2.5	582	2	US-09-543-681A-4556	Sequence 4556, Ap	1353	85	2.4	724	2	US-09-248-796A-18020	Sequence 12100, A
1281	86	2.5	591	2	US-09-489-039A-12837	Sequence 12837, A	1354	85	2.4	729	2	US-09-489-039A-19100	Sequence 12100, A
1282	86	2.5	631	2	US-09-134-001C-3843	Sequence 3843, Ap	1355	85	2.4	750	2	US-09-583-110-4010	Sequence 14943, A
1283	86	2.5	660	2	US-09-462-606-48	Sequence 48, Appl	1356	85	2.4	751	2	US-09-252-991A-133073	Sequence 33073, Ap
1284	86	2.5	705	2	US-09-902-540-11260	Sequence 11260, A	1357	85	2.4	827	3	US-10-171-384-3	Sequence 3, Appl1
1285	86	2.5	802	2	US-09-081-345-18	Sequence 18, Appl	1358	85	2.4	946	2	US-09-546-153-1	Sequence 1, Appl1
1286	86	2.5	802	2	US-09-822-295-18	Sequence 18, Appl	1359	85	2.4	1034	2	US-09-252-991A-26658	Sequence 26658, A
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1288	86	2.5	846	2	US-09-902-540-15310	Sequence 9924, Ap	1361	85	2.4	1289	1	US-07-675-772-4	Sequence 4, Appl1
1289	86	2.5	846	2	US-10-104-047-2444	Sequence 15310, A	1362	85	2.4	1289	1	US-08-063-170-4	Sequence 4, Appl1
1290	86	2.5	1000	2	US-09-193-562D-30	Sequence 30, Appl	1363	85	2.4	1289	1	US-08-158-232-4	Sequence 4, Appl1
1291	86	2.5	1000	2	US-10-035-412B-30	Sequence 30, Appl	1364	85	2.4	1289	1	US-08-304-626-4	Sequence 4, Appl1
1292	86	2.5	1127	2	US-09-150-460B-11	Sequence 11, Appl	1365	85	2.4	1289	1	US-08-316-301A-4	Sequence 4, Appl1
1293	86	2.5	1127	2	US-09-602-787A-54	Sequence 54, Appl	1366	85	2.4	1289	1	US-08-616-301A-4	Sequence 4, Appl1
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTTVLTMAKASVIEFVLVTGSHNKETAKIKRPKFTVQINCDAVAKIIDPEFV 60
DB 1 MTTVLTMAKASVIEFVLVTGSHNKETAKIKRPKFTVQINCDAVAKIIDPEFV 60
QY 61 KCPACGDPKHVYGTDVYASVYCGAAVHSGVLDNSGKILVRKVAQSGSKYSYNG 120
DB 61 KCPACGDPKHVYGTDVYASVYCGAAVHSGVLDNSGKILVRKVAQSGSKYSYNG 120
QY 121 VQSLSPWRRESFVILESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
DB 121 VQSLSPWRRESFVILESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
QY 121 VQSLSPWRRESFVILESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
DB 121 VQSLSPWRRESFVILESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIGTTAQ 180
QY 181 PVTLMQILAVTVAATPTTLPPSPSAASTTISIPRQSGHRSQEMDLMTATYSSQNR 240
DB 181 PVTLMQILAVTVAATPTTLPPSPSAASTTISIPRQSGHRSQEMDLMTATYSSQNR 240
QY 241 PRADGICRQDPSGAFOKPVGADVSLGLVPEKEISTQSLPEVSLGDPNCKIDSLFLDG 300
DB 241 PRADGICRQDPSGAFOKPVGADVSLGLVPEKEISTQSLPEVSLGDPNCKIDSLFLDG 300
QY 301 STSICKRRFRIOKOLADVAQALDIGPAPLMGVVOYGDNPATHTNLTHTNSRDLKTAI 360
DB 301 STSICKRRFRIOKOLADVAQALDIGPAPLMGVVOYGDNPATHTNLTHTNSRDLKTAI 360
QY 361 EKITORGGSINVGRAISFVTKNFFSKANGNSGANNVWVDGPTDKEASRLARES 420
DB 361 EKITORGGSINVGRAISFVTKNFFSKANGNSGANNVWVDGPTDKEASRLARES 420
QY 421 GINIFITTEGAENKQYVVEPNANKAVCTNGFYSILHQSNGLHKTIOPLVRCVCD 480
DB 421 GINIFITTEGAENKQYVVEPNANKAVCTNGFYSILHQSNGLHKTIOPLVRCVCD 480
QY 481 TDRLAASKTCLNSADIGFVLDGSSSVGTGNFETVLOFTNLTKFEISDTRIGAVOYT 540
DB 481 TDRLAASKTCLNSADIGFVLDGSSSVGTGNFETVLOFTNLTKFEISDTRIGAVOYT 540
QY 541 YEORLEFEGFDYSSKPDILNAIKRVYWSGGTSTGAALNFALEQLFKSKPKNRKMLLI 600
DB 541 YEORLEFEGFDYSSKPDILNAIKRVYWSGGTSTGAALNFALEQLFKSKPKNRKMLLI 600
QY 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAQBELVIAITHPADHSFFVDEPNLHOY 660
DB 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAQBELVIAITHPADHSFFVDEPNLHOY 660
QY 661 VPRIIIONICTEFSNOPS 678
DB 661 VPRIIIONICTEFSNOPS 678
RESULT 2
US-09-990-444-179
Sequence 179, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Auelin L.
APPLICANT: Kijavien, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zheng, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090540

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PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMTKASVIEMLVLLVTGHSNKEETAKKIKRPFVPOINCDVXAGKIIDPEFTV 60
1 MRTVLTMTKASVIEMLVLLVTGHSNKEETAKKIKRPFVPOINCDVXAGKIIDPEFTV 60
DB 61 KCPAGCQDPKYHYGGTDVYASYSVCGAIVHSGVLNDSGKILVRVACQSGYKGSYSNG 120
61 KCPAGCQDPKYHYGGTDVYASYSVCGAIVHSGVLNDSGKILVRVACQSGYKGSYSNG 120
QY 121 VQSLSPRMESEFVIESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPGTTAQ 180
121 VQSLSPRMESEFVIESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSPRMESEFVIESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPGTTAQ 180
121 VQSLSPRMESEFVIESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHSQEMDLNSTATYSSQNR 240
181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHSQEMDLNSTATYSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHSQEMDLNSTATYSSQNR 240
181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHSQEMDLNSTATYSSQNR 240
QY 241 PRADPGIQRODPGGAFFQKRVGADVSLGLVPEKELSTOSLEPVSLDDPNCIKIDLSFLDQ 300
241 PRADPGIQRODPGGAFFQKRVGADVSLGLVPEKELSTOSLEPVSLDDPNCIKIDLSFLDQ 300
DB 241 PRADPGIQRODPGGAFFQKRVGADVSLGLVPEKELSTOSLEPVSLDDPNCIKIDLSFLDQ 300
241 PRADPGIQRODPGGAFFQKRVGADVSLGLVPEKELSTOSLEPVSLDDPNCIKIDLSFLDQ 300
QY 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360
301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360
DB 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360
301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360
QY 361 EKITORGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVVMDGPTDVEASRLARBS 420
361 EKITORGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVVMDGPTDVEASRLARBS 420
DB 361 EKITORGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVVMDGPTDVEASRLARBS 420
361 EKITORGGLSNVGRALISFVTKNFSSKANGNSGAPNVVVVVMDGPTDVEASRLARBS 420
QY 421 GINIFITTEGAENKQYVVEBNPANKAVCRINGEYSILHVSQMPGLHHTIQPLVRYVCD 480
421 GINIFITTEGAENKQYVVEBNPANKAVCRINGEYSILHVSQMPGLHHTIQPLVRYVCD 480

Db 421 GINIFFITLEGAEKQYVWPNPANKAVCKTNGFYSLHVQSWGHLKHTIÖPLKRVCD 480
Qy 481 TDRLASCKTCLNSADIGFVIDGSSVGTGNFRTVQFVTNLTKFEISDTDRIGAVOYT 540
Db 481 TDRLASCKTCLNSADIGFVIDGSSVGTGNFRTVQFVTNLTKFEISDTDRIGAVOYT 540
Qy 541 YEORLEFGFDKYSKPDILMAIKRVGWSGCTSGAINFALBOLFKSKPKRKLMTLI 600
Db 541 YEORLEFGFDKYSKPDILMAIKRVGWSGCTSGAINFALBOLFKSKPKRKLMTLI 600
Qy 601 TDGRSYDVVRIPAMAHKGVTTVAIGVMAAOELEVIAITHPADHSFPVDEPNLHOY 660
Db 601 TDGRSYDVVRIPAMAHKGVTTVAIGVMAAOELEVIAITHPADHSFPVDEPNLHOY 660
Qy 661 VPRITONICTEFSNOPS 678
Db 661 VPRITONICTEFSNOPS 678
RESULT 3
US-09-997-333-179
Sequence 179, Application US/0997333
Patent No. 6853836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-17

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; PRIOR FILING DATE: 1998-07-09

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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 VQSLSLPRMRESFIVLESKPKKVTYPSALTYSSSSPAAQGETTKAQRPIPGTTAQ 180
DB      121 VQSLSLPRMRESFIVLESKPKKVTYPSALTYSSSSPAAQGETTKAQRPIPGTTAQ 180
QY      181 PVTLMQULAVTVAVATPTTLPRPSPAASTTSIPRQSGVGRSQEMDLSTATYTSQNR 240
DB      181 PVTLMQULAVTVAVATPTTLPRPSPAASTTSIPRQSGVGRSQEMDLSTATYTSQNR 240
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DB      241 PRADPGIORODPSGAAFOKRVGADVSLGLVPKEELSTOSLEPVSLDPPNCKIDLSFLIDG 300
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DB      301 STSGKRRRRIQOLLADVAQALDIPGAPPLMGVVOYGNPRAHFNULKTHYSRDLKTAI 360
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DB      421 GINIFFITTEGAENKQYVVEBNFANKAVCRITNGFSYLHVSQWFGIAKTLQPLVRVCD 480
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QY      661 VPRIONICTEFPNSOPRN 678
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrata, Napoleone
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; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Db 61 KCPAGCDPKYHVYGTVDVYASYSVCGAAVHSGVLDNSGKILVRKVAQSGYKYSNG 120

Qy 121 VQSLSTRMRRESFVLESKPKKGTTPSALTYSKSPAAQAGTTTAAQRPPIPTTAAQ 180
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Db 181 PVTLMOLLAVVAATPTTLPRPSPSAATSTSIIRPOSVGHRSQEMDMSTATTSSQNR 240

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Db 241 PRADPGIQRODPSGAAPFQKPVGADVSLGLVKEELSTQSLPEVSLGDPNCKIDLSPLIDG 300

Qy 301 STSISGKRRFRIOKQLADVQAALDIGPAGPLMGVVOYGDNPATFHNKITHNSRDLXTAI 360
Db 301 STSISGKRRFRIOKQLADVQAALDIGPAGPLMGVVOYGDNPATFHNKITHNSRDLXTAI 360

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/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Bastein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gertlisen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gunney, Austin L.
/ APPLICANT: Kijavian, Ivar J.
/ APPLICANT: Napier, Mary A.
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/ APPLICANT: Paoni, Nicholas F.
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/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
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/ CURRENT APPLICATION NUMBER: US/09/989, 735
/ CURRENT FILING DATE: 2001-11-19
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73	PRIOR APPLICATION NUMBER: 60/089653

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65	PRIOR FILING DATE: 1998-07-02	
66	PRIOR APPLICATION NUMBER: 60/091978	
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0;
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 QY 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDSSGKILVRKVAAGSGYKGSYNG 120
 DB 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDSSGKILVRKVAAGSGYKGSYNG 120
 QY 121 VQSLSPRMBESFVLESKPKKGYTPSALTYSKSKSPAQAQETTYAYQRPPIGTAAQ 180
 DB 121 VQSLSPRMBESFVLESKPKKGYTPSALTYSKSKSPAQAQETTYAYQRPPIGTAAQ 180
 QY 181 PVTLMOALATVAATPTLLPRSPSAASTTSIPRPSVGHRSQEMLMSTATVTSQNR 240
 DB 181 PVTLMOALATVAATPTLLPRSPSAASTTSIPRPSVGHRSQEMLMSTATVTSQNR 240
 QY 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
 DB 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
 QY 301 STSGKRRFRIOKOLLADVAQALDIGAPGLMGVVOYQDNPAITHFNILKTHNSRDLKTAI 360
 DB 301 STSGKRRFRIOKOLLADVAQALDIGAPGLMGVVOYQDNPAITHFNILKTHNSRDLKTAI 360
 QY 361 EKITRGGLSNVGRISFVTNKFPSKANGNSGAPNVVVVWDMPDVKYEEASRLRES 420
 DB 361 EKITRGGLSNVGRISFVTNKFPSKANGNSGAPNVVVVWDMPDVKYEEASRLRES 420
 QY 421 GINIFITIEGAANEKOYVEPNFANKAVCRTPFYSLSHVOSFGLHKTLOPLVKEVCD 480
 DB 421 GINIFITIEGAANEKOYVEPNFANKAVCRTPFYSLSHVOSFGLHKTLOPLVKEVCD 480
 QY 481 TDRACSKTCLNSADIGFVIDGSSVGTGNFRYLOVYTNLTKEFEISDPTDRGAVOYT 540
 DB 481 TDRACSKTCLNSADIGFVIDGSSVGTGNFRYLOVYTNLTKEFEISDPTDRGAVOYT 540
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 QY 601 TDGRSYDVRIIPAMAHLKGVITYAIGVAMAQEELEVIATHPARDHSFVDEFDNLHOY 660
 DB 601 TDGRSYDVRIIPAMAHLKGVITYAIGVAMAQEELEVIATHPARDHSFVDEFDNLHOY 660
 QY 661 VPRIIIONICTEFNSQPRN 678
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 US-09-989-726-179
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 ; Patent No. 7018811
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Maty E.
 ; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P27301C60
 ; CURRENT APPLICATION NUMBER: US/09/989,726
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
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DB 61 KCPAGCOPPKYHYGTDVVASYSGCAAVHSGVLNDSGGKILVRKVGOSGYKGSYSG 120
QY VQSLSPRMRESFIVLESKRKKGVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSPRMRESFIVLESKRKKGVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
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DB 181 PVTLMOLLAVTVAVAPPTLIPRPSAASSTISIPRPOSVGHRSQEMDLWSTATYTSQNR 240
QY PRADPGIORODPSGAFQKRVGADVSLGLVPKXELSTOSLEPVSLDPPNCKIDLSFLIDG 300
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QY STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGPNPATHFNLKTHNSRDLKTAI 360
DB 301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGPNPATHFNLKTHNSRDLKTAI 360
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QY 481 TDRIACSKTCLNSADIGFVIDGSSVGTGNFRVLQFVNLTKFEFISDTRIGAVOYT 540
Db 481 TDRIACSKTCLNSADIGFVIDGSSVGTGNFRVLQFVNLTKFEFISDTRIGAVOYT 540
QY 541 YEORLFEPKYSKSPILNAIKRVGWGSGTSGAINFALBQLFKSKPKNRKMTLI 600
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Db 601 TDSRSYDVARIIPMAAHAKGVITVIAIGVANAQOELEVIATHPARDSFVDEEDNLHQY 660
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Db 661 VPRIIQNICTEFNSQPRN 678

RESULT 7
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Sequence 179, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/997,514
PRIOR FILING DATE: 2001-11-15
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 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
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 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMKASVIMFLVLTGTHSNKETAKKIKRPFYVPOINCDVYKAKIIDPEITV 60
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 QY KCPAGCDDPKYHVGTVDVYASVSSVCGAAVHSGVLDNSGKILVRKAYAGSGYSGYSNG 120
 DB KCPAGCDDPKYHVGTVDVYASVSSVCGAAVHSGVLDNSGKILVRKAYAGSGYSGYSNG 120
 QY 121 VQSLPRMRBSFVLESKPKKVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
 DB 121 VQSLPRMRBSFVLESKPKKVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
 QY 181 PVTLMQLLAVTVAVATPTTLPREPSPAATSTIRPQSVGHRSGEMDLMSTATTSSQNR 240
 DB 181 PVTLMQLLAVTVAVATPTTLPREPSPAATSTIRPQSVGHRSGEMDLMSTATTSSQNR 240
 QY 241 PRADPGIORODPSGAAPKPGADVSLGLVPKEELSTQSLPEVSLGPNCIKIDSLFIDG 300
 DB 241 PRADPGIORODPSGAAPKPGADVSLGLVPKEELSTQSLPEVSLGPNCIKIDSLFIDG 300
 QY 301 STSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSBDLKTAI 360
 DB 301 STSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSBDLKTAI 360
 QY 361 EKIQRGSLNMGALISFVTKNPFSSKANGRSGAPNVMVWGDMPDKVEASRLRES 420
 DB 361 EKIQRGSLNMGALISFVTKNPFSSKANGRSGAPNVMVWGDMPDKVEASRLRES 420
 QY 421 GINIFFTTIGAAENEQYVVEPNFANKAVCRTGFGYSLHVSFGJHKTLOPLVKEVCD 480
 DB 421 GINIFFTTIGAAENEQYVVEPNFANKAVCRTGFGYSLHVSFGJHKTLOPLVKEVCD 480
 QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFTNLTKFEISDTRIGAVOYT 540
 DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFTNLTKFEISDTRIGAVOYT 540
 QY 541 YEQRLFGFDPKYSKPIILNAIKRVGWSGTSFGAIALNBOLFKKSKPNKRMILI 600
 DB 541 YEQRLFGFDPKYSKPIILNAIKRVGWSGTSFGAIALNBOLFKKSKPNKRMILI 600
 QY 601 TDGRSYDVARIPMAAHLKGVITTAIGVMAAOBELVIAHTPARDSFFVDEEDNLHOY 660
 DB 601 TDGRSYDVARIPMAAHLKGVITTAIGVMAAOBELVIAHTPARDSFFVDEEDNLHOY 660
 QY 661 VPRILQICTEFNSQPN 678
 DB 661 VPRILQICTEFNSQPN 678

RESULT 8
 US-09-989-728-179
 Sequence 179, Application us/09989728
 Patent No. 7029873
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gettitsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTKKASVIMFLVLTGVHSNKTAKTKRPFVTPQINCVDYKAKIIDPEFIV 60
DB 1 MRTVVLTKKASVIMFLVLTGVHSNKTAKTKRPFVTPQINCVDYKAKIIDPEFIV 60
QY 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDSGGKILVRKTVAGOSGYGYSNG 120
DB 61 KCPAGCDDPKHYVGTVDVYASYSVCGAAVHSGVLNDSGGKILVRKTVAGOSGYGYSNG 120
QY 121 VQSLPRMRESFVLESKPKKGYTYSALTYSKSPKPAAGETTRAYORPPIPGTTAAQ 180
DB 121 VQSLPRMRESFVLESKPKKGYTYSALTYSKSPKPAAGETTRAYORPPIPGTTAAQ 180
QY 181 PVTLMQLLAVTVAATPTTLPRSPSASTTSIRPQSVGHRSGEMLMSTAYTSSQNR 240
DB 181 PVTLMQLLAVTVAATPTTLPRSPSASTTSIRPQSVGHRSGEMLMSTAYTSSQNR 240
QY 241 PRADPGIQRDPSGAFOKPYGAVVSLGLVPEKELSQSLPEVSLGDPNCKIDLSFLIDG 300
DB 241 PRADPGIQRDPSGAFOKPYGAVVSLGLVPEKELSQSLPEVSLGDPNCKIDLSFLIDG 300
QY 301 STSIGKRFRIOKOLLADVAQALDIPAGPLMGVVOYGDNPATHFNLKTHNSRDLKTAI 360
DB 301 STSIGKRFRIOKOLLADVAQALDIPAGPLMGVVOYGDNPATHFNLKTHNSRDLKTAI 360
QY 361 EKTIRGRLSNVGAISFTVTNPFSSKNGNRSGAPNVVVVWVGMPDXTKEASRLARES 420

DB 361 EKTIRGRLSNVGAISFTVTNPFSSKNGNRSGAPNVVVVWVGMPDXTKEASRLARES 420
QY 421 GINIFPTTIGCAENESQYVEPFAFKAVCRNTNGFYSLHVQSWFGHAKTLQPLVKRVC 480
DB 421 GINIFPTTIGCAENESQYVEPFAFKAVCRNTNGFYSLHVQSWFGHAKTLQPLVKRVC 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFTVNLTKFEISDTRIGAVOYT 540
DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFTVNLTKFEISDTRIGAVOYT 540
QY 541 YEORLEFGFDKYSKPDILNAIKRVGWSGCTSGAAINFALBOLFCKSKPNRKKMLILI 600
DB 541 YEORLEFGFDKYSKPDILNAIKRVGWSGCTSGAAINFALBOLFCKSKPNRKKMLILI 600
QY 601 TDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVITHPARDHSFPVDEFDNLHOY 660
DB 601 TDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVITHPARDHSFPVDEFDNLHOY 660
QY 661 VPRIIQNICTEFNSQPRN 678
DB 661 VPRIIQNICTEFNSQPRN 678

RESULT 9
US-09-997-349-179
Sequence 179, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

1 PRIOR APPLICATION NUMBER: 60/084600
2 PRIOR FILING DATE: 1998-05-07
3 PRIOR APPLICATION NUMBER: 60/087106
4 PRIOR FILING DATE: 1998-05-28
5 PRIOR APPLICATION NUMBER: 60/087607
6 PRIOR FILING DATE: 1998-06-02
7 PRIOR APPLICATION NUMBER: 60/087609
8 PRIOR FILING DATE: 1998-06-02
9 PRIOR APPLICATION NUMBER: 60/087759
10 PRIOR FILING DATE: 1998-06-02
11 PRIOR APPLICATION NUMBER: 60/087827
12 PRIOR FILING DATE: 1998-06-03
13 PRIOR APPLICATION NUMBER: 60/088021
14 PRIOR FILING DATE: 1998-06-04
15 PRIOR APPLICATION NUMBER: 60/088025
16 PRIOR FILING DATE: 1998-06-04
17 PRIOR APPLICATION NUMBER: 60/088026
18 PRIOR FILING DATE: 1998-06-04
19 PRIOR APPLICATION NUMBER: 60/088028
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21 PRIOR APPLICATION NUMBER: 60/088029
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23 PRIOR APPLICATION NUMBER: 60/088030
24 PRIOR FILING DATE: 1998-06-04
25 PRIOR APPLICATION NUMBER: 60/088033
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28 PRIOR FILING DATE: 1998-06-04
29 PRIOR APPLICATION NUMBER: 60/088167
30 PRIOR FILING DATE: 1998-06-05
31 PRIOR APPLICATION NUMBER: 60/088202
32 PRIOR FILING DATE: 1998-06-05
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35 PRIOR APPLICATION NUMBER: 60/088217
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38 PRIOR FILING DATE: 1998-06-09
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53 PRIOR APPLICATION NUMBER: 60/088861
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56 PRIOR FILING DATE: 1998-06-11
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYVLMKASYIEMLVLTGVSNKETAKIKRPETVQINCDVAKGIIIDPEIV 60
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QY 61 KCPAGCOPKXHVYTDVYASYSVCGAAVHSGVLDNCGKILVKKVAGSGYKSYNG 120
DB 61 KCPAGCOPKXHVYTDVYASYSVCGAAVHSGVLDNCGKILVKKVAGSGYKSYNG 120
QY 121 VQSLSPWRRESFVLESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIGTTAQ 180
DB 121 VQSLSPWRRESFVLESKPKKGVTPSALTYSKSPAAOAGETTKAYORPPIGTTAQ 180
QY 181 PVTLMQLLAVVAATPTTLPRPSPASTSIPRPOVGRHSQMDLWSTATTYSSQNR 240
DB 181 PVTLMQLLAVVAATPTTLPRPSPASTSIPRPOVGRHSQMDLWSTATTYSSQNR 240
QY 241 PRADPGIOROPSGAFOKPVGADVSLGVPEEELSTOSLEPVSLGDNCKIDLSFLIDG 300
DB 241 PRADPGIOROPSGAFOKPVGADVSLGVPEEELSTOSLEPVSLGDNCKIDLSFLIDG 300
QY 301 STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVQYQDNPDATHFNLTHTNSDLKTAI 360
DB 301 STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVQYQDNPDATHFNLTHTNSDLKTAI 360
QY 361 EKITORGGLSNVGRASIVTKNFPKANGNSGAPNVVVVNDGPTPKVEASRLAES 420
DB 361 EKITORGGLSNVGRASIVTKNFPKANGNSGAPNVVVVNDGPTPKVEASRLAES 420
QY 421 GINIFITIEGAENKQYVVEPNFANKAVCRINGFSLHYQSMFGHLTKIOLPKVRCV 480
DB 421 GINIFITIEGAENKQYVVEPNFANKAVCRINGFSLHYQSMFGHLTKIOLPKVRCV 480
QY 481 TDRIACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKHEEISDTOTRI GAVOYT 540
DB 481 TDRIACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKHEEISDTOTRI GAVOYT 540
QY 541 YEOGLERFQDKSSKPDILNAIKRVGYSGSTSGAINEFLBOLFKSKENKKTMLTI 600
DB 541 YEOGLERFQDKSSKPDILNAIKRVGYSGSTSGAINEFLBOLFKSKENKKTMLTI 600
QY 601 TDGSSYDDVRI PAMAAMHKGIVITTAIGVMAAOELEVIAIHPARDHSFFVDEFDNLHOY 660
DB 601 TDGSSYDDVRI PAMAAMHKGIVITTAIGVMAAOELEVIAIHPARDHSFFVDEFDNLHOY 660
QY 661 VPRIIIONICTEFSQPRN 678
DB 661 VPRIIIONICTEFSQPRN 678

RESULT 10

US-09-997-653-179
Sequence 179, Application US/09997653
Patent No. 7034122

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTMKASVIEMLVLLVTGVHSNKEITAKKIRKPKFTVPQINCVDYKAGIIDEPIY 60
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DB 61 KCPAGCQDPKHYHYGDDVYASYSVCGAAVHSGVLNDSGKILVRVAQSGYKGSYSNG 120
61 KCPAGCQDPKHYHYGDDVYASYSVCGAAVHSGVLNDSGKILVRVAQSGYKGSYSNG 120

QY 121 VQSLSPRRRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPIPGTTAQ 180
121 VQSLSPRRRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPIPGTTAQ 180

DB 121 VQSLSPRRRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPIPGTTAQ 180
121 VQSLSPRRRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPIPGTTAQ 180

QY 181 PVTLMQLLAVTAVATPTLLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240
181 PVTLMQLLAVTAVATPTLLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240

DB 181 PVTLMQLLAVTAVATPTLLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240
181 PVTLMQLLAVTAVATPTLLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240

QY 241 PRADPGIORODPSGAFQKPVGADVSLGVPKKEELSTQSLPEVSLGDPNCKIDLSTFLIG 300
241 PRADPGIORODPSGAFQKPVGADVSLGVPKKEELSTQSLPEVSLGDPNCKIDLSTFLIG 300

DB 241 PRADPGIORODPSGAFQKPVGADVSLGVPKKEELSTQSLPEVSLGDPNCKIDLSTFLIG 300
241 PRADPGIORODPSGAFQKPVGADVSLGVPKKEELSTQSLPEVSLGDPNCKIDLSTFLIG 300

QY 301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGNPAPHFLIKHTNSRDLKTAI 360
301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGNPAPHFLIKHTNSRDLKTAI 360

DB 301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGNPAPHFLIKHTNSRDLKTAI 360
301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGNPAPHFLIKHTNSRDLKTAI 360

QY 361 EKITORGGLSNVGRALSFVTKNFFSKANGNSGAPNVVVVWDGPTDVEASRLAERS 420
361 EKITORGGLSNVGRALSFVTKNFFSKANGNSGAPNVVVVWDGPTDVEASRLAERS 420

Db 361 EKTORGGISNVGRALISFVTKNFFSKANGNRSGANVWVWDGPTDKVEASRLARES 420
Qy 421 GINIFITITEGAAENKQVYVPEPNFANKAVCTNGFYSLHVOSFGLKHTLOPLKRYCD 480
Db 421 GINIFITITEGAAENKQVYVPEPNFANKAVCTNGFYSLHVOSFGLKHTLOPLKRYCD 480
Qy 481 TDRLACSKTCLNSADIGFVNDGSSSVGTGNFRVTLQFVNTLTKEREISDTRIGAVOYT 540
Db 481 TDRLACSKTCLNSADIGFVNDGSSSVGTGNFRVTLQFVNTLTKEREISDTRIGAVOYT 540
Qy 541 YEORLEFEGFDKXSSKPDILNAIKRQYWSGGTSTAANFALBQLFKSKPKRKLMTLI 600
Db 541 YEORLEFEGFDKXSSKPDILNAIKRQYWSGGTSTAANFALBQLFKSKPKRKLMTLI 600
Qy 601 TDGSSYDVDRIPAMAHLKGVITYAIGVMAAOELEVATYTHPARDSFPVDEPDNLHQY 660
Db 601 TDGSSYDVDRIPAMAHLKGVITYAIGVMAAOELEVATYTHPARDSFPVDEPDNLHQY 660
Qy 661 VPRITIIIONICTEFSNSOPRN 678
Db 661 VPRITIIIONICTEFSNSOPRN 678

RESULT 11

US-09-989-293A-179
Sequence 179, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/087106
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 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090690
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090694
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633

; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTVLTMAKASVEMFLVLLVTGSHNKETAKKIKKPKFTVPQINDVYAGKIIDEEFIY 60
 DB 1 MRTVLTMAKASVEMFLVLLVTGSHNKETAKKIKKPKFTVPQINDVYAGKIIDEEFIY 60
 QY 61 KCPAGCQDPKHYHYGVGVVYASYSVCGAAVHSGVLNNGSKILLRVAGQSGYKGSYSNG 120
 DB 61 KCPAGCQDPKHYHYGVGVVYASYSVCGAAVHSGVLNNGSKILLRVAGQSGYKGSYSNG 120
 QY 121 VQSLSLPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQ 180
 DB 121 VQSLSLPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQ 180
 QY 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHRQEMDLWSTATYTSQNR 240
 DB 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSIPRQSVGHRQEMDLWSTATYTSQNR 240
 QY 241 PRADPGIQRODPBGAAFOKRVGVADVSLGVLPKKELSLQSLSEPLSLDDPNCKIDLSEFLIOG 300
 DB 241 PRADPGIQRODPBGAAFOKRVGVADVSLGVLPKKELSLQSLSEPLSLDDPNCKIDLSEFLIOG 300
 QY 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVQYGNPAPHNLKHTNSRDLKTAI 360
 DB 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVQYGNPAPHNLKHTNSRDLKTAI 360
 QY 361 EKITQRGGLSNVGRASIVTNTKFFSKANGNSGAPVVVVVMDVDPDVEASRLARES 420
 DB 361 EKITQRGGLSNVGRASIVTNTKFFSKANGNSGAPVVVVVMDVDPDVEASRLARES 420
 QY 421 GINIFITTEGAENKQYVEPNFANKAVCRNGYSYLHVQSPGLHTLQGLVVRVD 480
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 QY 481 TDRLASCKTCLNSADIGFVIDGSSVGTGNFRVLQFVNLTKEFEISDTRIGAVOYT 540
 DB 481 TDRLASCKTCLNSADIGFVIDGSSVGTGNFRVLQFVNLTKEFEISDTRIGAVOYT 540
 QY 541 YEQRLEFGDPKYSKPDILINAIKRVGVSGSTSGAINFALBQLFKSKPNKRKLMILI 600
 DB 541 YEQRLEFGDPKYSKPDILINAIKRVGVSGSTSGAINFALBQLFKSKPNKRKLMILI 600
 QY 601 TDRGSYDVARIPMAHLKGVLTAYAGVMAAELEVLATHPARHSPFVDEFDLHOV 660
 DB 601 TDRGSYDVARIPMAHLKGVLTAYAGVMAAELEVLATHPARHSPFVDEFDLHOV 660
 QY 661 VPRIIIONICTEFSQPRN 678
 DB 661 VPRIIIONICTEFSQPRN 678
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 US-09-907-794A-227
 ; Sequence 227, Application US/09907794A
 ; Patent No. 6635468
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen


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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-227
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Query Match          32.3%; Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7,

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Db 32 ITCTRGIDIRKADVLCPGGCPLSESVYGNIVVSSICGAHVAGVISNSGQVVR 91
QY 104 VRKAVGSGYKGSNGVQSLSPWRBSFVLVLSKPKGVYTSALTYSKSPAAQAG 163
Db 92 VYSLPGRENVSSVANGIQSQMLSRWSASFVTYKTK-----SSTQATQGA- 137
QY 164 ETTAVYORPPIPGTTAQVTLMLLAATVAATPTTLPRPSPASTTISIRPQSVGRS 223
Db 138 -----VSTPAH----- 143
QY 224 QEMDLWSTATVYTSQNRPRADPGIQRDPGSAFAQKPVGADVSLGLVPEKELSTQSLPEV 283
Db 144 -----PTGKRLLK-----TPKK----- 156
QY 284 SLGPNCKIDSLFIDGSTIGKRRFRIQKQLADVQAOLDIGAPGLMGVGVGDNPAT 343
Db 157 -TGKDCADIAFLIDGSEFNIGORFNIQKNFVKVLMIGIGTEGPHVGLVQASEHPXI 215
QY 344 HFNKTHNSRDLTKATEKINQRGSLNVGRALISFVTKNFSKXANGNSGAPNVVVMVD 403
Db 216 EFTYKNTSADVLPAKEVGFGRGNSNTGKALKHTAQKFTVDAGVRKGIPIKVVVVID 275
QY 404 GMPPTDVEASRLARESGINIFFTIEGAANEKQVVEPFPANKAVCRTGTFYSLHVS 463
Db 276 GWPEDDIEBAGIVAREFGVNVFIVSAKPIPEELGMQDVTYFVDAKACRRNNGFSYMPN 335
QY 464 WFGIHLKLOPLVKVYCTDLRACSKTCLNSADIGFVIDGSSSVGTGNFRVYLOFVNLTK 523
Db 336 WFGITKVKVPLVQKLCHEQMMCKCTCNYSVINFLIDGSSSVSDSNFRMLLEFVSNIAK 395
QY 524 EPEISDTRIGAVQYVTEORLEFGPKYSKPIULNAIKRVGWSGTSGAALNPALE 583
Db 396 TFEISDYGAKIAAQQFTYDQRTESFTDYSTKEVNLAVIRKIRIWSGSLATGDAISFTVR 455
QY 584 QLFK-KSKPNKRLMLITDGRSYDVDRIPAMAHLKGVITVAIGVMAAQEELVIAT 641
Db 456 NVFPIRESPPK-NEFVITVDGQSYDDVQGPAAAHAGITFISVGVAMAPLDLKMAS 514
QY 642 HPADHSFPVDEPNLQVYPRITQNTCTER 672
Db 515 KPKEASHAFTRFGLPIVSDVIRGICRDP 545
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RESULT 15
US-09-906-700-227

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; Sequence 227, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-227
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GenCore version 5.1.9
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OM protein - protein search, using SW model

Run on: September 5, 2006, 20:00:53 ; Search time 306 Seconds
(without alignments)
2049.544 Million cell updates/sec

Title: US-10-063-538-34

Perfect score: 3502
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Scoring table: BLOSUM62
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Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3484.5	99.5	693	2	Q9UDN0_HUMAN
3	3344	95.5	656	2	Q96DT1_HUMAN
4	2826	80.7	650	2	Q3T247_MOUSE
5	2823	80.6	650	2	Q8VHT5_MOUSE
6	2818	80.5	652	2	Q95L12_BOVIN
7	2801	80.0	650	2	Q8K047_MOUSE
8	2796	79.8	650	2	Q9CY21_MOUSE
9	2682	76.6	628	2	Q8BQ41_MOUSE
10	2311.5	66.0	748	2	Q5NTW9_CHICK
11	1929	55.1	680	2	Q4RP27_TETNG
12	1187.5	33.9	553	2	Q8AM56_BRARE
13	1139	32.5	547	1	COCH_HUMAN
14	1129.5	32.3	550	1	COCH_CHICK
15	1123.5	32.1	550	2	Q5EA64_BOVIN
16	1115	31.8	552	2	Q3U021_MOUSE
17	1113	31.8	552	1	COCH_MOUSE
18	1113	31.8	552	2	Q3TAF5_MOUSE
19	1017.5	29.1	494	2	Q96I06_HUMAN
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24	552	15.8	3119	1	COCA1_MOUSE
25	543.5	15.5	3063	1	COCA1_HUMAN
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33	494.5	14.1	498	2	Q5X124_RAT	Q5X124 rattus norv
34	493	14.1	500	2	Q80V55_MOUSE	Q80V55 mus musculus
35	490	14.0	493	1	MATN1_CHICK	P05039 gallus gall
36	490	14.0	500	1	MATN1_MOUSE	P51942 mus musculu
37	488.5	13.9	1259	2	Q4RPI2_TETNG	Q4RPI2 tetraodon n
38	485	13.8	507	2	Q7ZVP3_BRARE	Q7ZVP3 brachydanio
39	478.5	13.7	644	2	Q5NJU1_BRARE	Q5NJU1 brachydanio
40	471.5	13.5	2588	2	Q53QF4_HUMAN	Q53QF4 homo sapien
41	471.5	13.5	3176	1	CO6A3_HUMAN	P12111 homo sapien
42	466	13.3	3169	2	Q4KRT6_CANFA	Q4KRT6 canis fami
43	464	13.2	1453	2	Q4RNL1_TETNG	Q4RNL1 tetraodon n
44	463	13.2	1182	2	Q8C6K9_MOUSE	Q8C6K9 mus musculu
45	459	13.1	685	2	Q5NJU2_BRARE	Q5NJU2 brachydanio
46	446.5	12.7	647	2	Q4S2X7_TETNG	Q4S2X7 tetraodon n
47	439.5	12.5	726	2	Q5NJU4_BRARE	Q5NJU4 brachydanio
48	435.5	12.4	1703	2	Q9Z019_MOUSE	Q9Z019 mus musculu
49	432.5	12.4	1636	2	Q4TBC0_TETNG	Q4TBC0 tetraodon n
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51	416.5	11.9	1222	2	Q63HQ4_HUMAN	Q63HQ4 homo sapien
52	415.5	11.9	1723	2	Q4SD22_TETNG	Q4SD22 tetraodon n
53	412.5	11.8	624	1	MATN4_MOUSE	Q89029 mus musculu
54	403.5	11.5	821	2	Q6PYX2_BRARE	Q6PYX2 brachydanio
55	400.5	11.4	2225	2	Q4SKX3_TETNG	Q4SKX3 tetraodon n
56	385.5	11.0	4421	2	Q4RK60_TETNG	Q4RK60 tetraodon n
57	380.5	10.9	840	2	Q32NR2_TETNG	Q32NR2 xenopus lae
58	378	10.8	790	2	Q6DCQ6_XENLA	Q6DCQ6 xenopus lae
59	378	10.8	2657	2	Q88493_MOUSE	Q88493 mus musculu
60	369.5	10.6	839	2	Q6P3N7_XENTR	Q6P3N7 xenopus tro
61	357.5	10.2	956	1	MATN2_HUMAN	Q00339 homo sapien
62	352.5	10.1	349	2	Q4SB12_TETNG	Q4SB12 tetraodon n
63	350.5	10.0	955	2	Q5R9N1_PONPY	Q5R9N1 pongo pygma
64	350.5	10.0	1797	1	COEAL1_MOUSE	Q80X19 mus musculu
65	343.5	9.8	717	2	Q4RG72_TETNG	Q4RG72 tetraodon n
66	342	9.8	944	2	Q5NUJ5_BRARE	Q5NUJ5 brachydanio
67	341	9.7	534	2	Q4G0W3_HUMAN	Q4G0W3 homo sapien
68	341	9.7	1796	1	COEAL1_HUMAN	Q05707 homo sapien
69	339.5	9.7	956	2	Q99K64_MOUSE	Q99K64 mus musculu
70	338.5	9.7	919	2	Q75RS52_LYMST	Q75RS52 Lymanaea sta
71	337.5	9.6	928	2	Q3T080_MOUSE	Q3T080 mus musculu
72	337.5	9.6	937	2	Q563V0_MOUSE	Q563V0 mus musculu
73	337.5	9.6	956	1	MATN2_MOUSE	Q08746 mus musculu
74	337.5	9.6	956	2	Q8R542_MOUSE	Q8R542 mus musculu
75	334	9.5	721	2	Q8CE01_MOUSE	Q8CE01 mus musculu
76	334	9.5	791	2	Q7UW27_MOUSE	Q7UW27 mus musculu
77	333	9.5	791	2	Q3UW88_MOUSE	Q3UW88 mus musculu
78	332.5	9.5	725	2	Q6Z539_HUMAN	Q6Z539 mus musculu
79	331	9.5	1888	1	COEAL1_HUMAN	Q26839 homo sapien
80	329.5	9.4	2944	1	CO7A1_HUMAN	P32018 gallus gall
81	326.5	9.3	950	2	Q4RK59_TETNG	Q4RK59 tetraodon n
82	326	9.3	1253	2	Q97566_CANFA	Q97566 canis fami
83	326	9.3	2936	2	Q7YRK8_CANFA	Q7YRK8 canis fami
84	325.5	9.3	725	2	Q6ZM07_HUMAN	Q6ZM07 homo sapien
85	325.5	9.3	755	2	Q5GFL6_HUMAN	Q5GFL6 homo sapien
86	325.5	9.3	755	2	Q70U28_HUMAN	Q70U28 homo sapien
87	324	9.3	2944	2	Q63870_MOUSE	Q63870 mus musculu
88	323	9.2	517	2	Q43853_HUMAN	Q43853 homo sapien
89	314.5	9.0	688	2	Q4TKK3_TETNG	Q4TKK3 tetraodon n
90	313	8.9	453	2	Q8TSC2_MYTGA	Q8TSC2 mytilus gal
91	310.5	8.9	565	2	Q18048_CABEL	Q18048 caenorhabdi
92	307	8.8	444	2	Q8TSC3_MYTED	Q8TSC3 mytilus edu
93	305	8.7	428	2	Q5NUJ0_BRARE	Q5NUJ0 brachydanio
94	300	8.6	441	2	Q8TEU5_MYTED	Q8TEU5 mytilus edu
95	299.5	8.6	1450	2	Q4RPI4_TETNG	Q4RPI4 tetraodon n
96	298	8.5	537	2	Q96A40_HUMAN	Q96A40 homo sapien
97	296	8.5	261	2	Q5CZ06_BRARE	Q5CZ06 brachydanio
98	295	8.4	1557	2	Q4SH63_TETNG	Q4SH63 tetraodon n
99	291.5	8.3	2101	2	Q61XK2_CABER	Q61XK2 caenorhabdi
100	290.5	8.3	954	2	Q8XKV8_HUMAN	Q8XKV8 homo sapien
101	290.5	8.3	957	2	Q9H0V3_HUMAN	Q9H0V3 homo sapien
102	290.5	8.3	957	2	Q96P44_HUMAN	Q96P44 homo sapien
103	289.5	8.3	957	2	Q8NFW1_HUMAN	Q8NFW1 homo sapien
104	287	8.2	1380	2	Q4S053_TETNG	Q4S053 tetraodon n

105	285.5	8.2	277	2	05N0K2_BRARE	05njk2 brachydanio	178	244.5	7.0	415	2	02MDK8_9EUTH	02mdk8 hemiceutete
106	284.5	8.1	441	2	04RNV3_TETNG	04rnv3 tetraodon n	179	244.5	7.0	419	2	07YRS0_MACCU	07yrs0 macaca mula
107	282.5	8.1	2813	1	VWF_MOTSE	08c1n3 mus musculu	180	244.5	7.0	427	2	028792_PANTR	028792 pan troglod
108	282.5	8.1	2813	2	0210J7_MOUSE	0210j7 mus musculu	181	244	7.0	421	2	09Z0R3_APIRU	09z0r3 aplodontia
109	282.5	8.1	2813	2	0210J8_MOUSE	0210j8 mus musculu	182	243.5	7.0	344	2	07Y0Y1_PHACT	07y0y1 phascolarct
110	281.5	8.1	293	2	05N0J3_BRARE	05njj3 brachydanio	183	243.5	7.0	411	2	08MWS8_TRIMA	08mws8 trichechus
111	281.5	8.0	409	2	04TJ70_TETNG	04tj70 tetraodon n	184	243.5	7.0	1151	2	09J1J30_RAT	09j1j30 rattus norv
112	281	8.0	320	2	05N0J4_BRARE	05njj4 brachydanio	185	243	6.9	425	2	028759_PROCA	028759 procavia ca
113	281	8.0	1472	2	090ZAO_CHICK	090zao gallus gall	186	242.5	6.9	344	2	086621_VOMUR	086621 vomeris
114	280.5	8.0	929	1	COCAI_NOTVI	091450 nophthalm	187	242.5	6.9	385	2	091YG0_MYSAL	091yg0 myseromys ur
115	280	8.0	957	2	0641F3_XENLA	0641f3 xenopus lae	188	242.5	6.9	413	2	07YRS2_HYLLA	07yrs2 hyllobates l
116	280	8.0	3770	2	061TH1_CAEBR	061th1 caenorhabdi	189	242.5	6.9	416	2	07YRS1_9PRIM	07yrs1 ceratopithec
117	279	8.0	2104	2	021281_CAEBL	021281 caenorhabdi	190	242	6.9	366	2	028639_RABIT	028639 oryctolagus
118	279	8.0	2104	2	0964N4_CAEBL	0964n4 caenorhabdi	191	242	6.9	414	2	07YRS4_PITPY	07yrs4 pithecia pi
119	279	8.0	3767	1	MU43_CAEBL	054576 caenorhabdi	192	242	6.9	418	2	09EPN5_HYDHY	09epn5 hydrochoeru
120	277.5	7.9	1702	2	059F25_HUMAN	059f25 homo sapien	193	241.5	6.9	385	2	091YB1_9RODE	091yb1 dasproctomys
121	276.5	7.9	548	2	05N0J3_BRARE	05njj3 brachydanio	194	241.5	6.9	417	2	060508_9HYST	060508 dasprocta
122	276	7.9	337	2	068EK6_BRARE	068ek6 brachydanio	195	241.5	6.9	421	2	09EPN3_MYOCO	09epn3 myocastor c
123	276	7.9	454	2	05TYX4_BRARE	05tyx4 brachydanio	196	241.5	6.9	2813	1	VWF_CANPA	028295 canis famli
124	273	7.8	299	2	05N0J7_BRARE	05njj7 brachydanio	197	241	6.9	385	2	091YF6_MICMN	091yf6 micromys mi
125	271.5	7.8	419	2	097925_MAGGI	097925 macropus gi	198	241	6.9	391	2	07YRM9_9EUTH	07yrm9 rhynchocyon
126	271	7.7	549	2	002808_BOVIN	002808 bos taurus	199	241	6.9	410	2	08S018_TENEC	08s018 tenrec ecan
127	270	7.7	299	2	03B7R3_BRARE	03b7r3 brachydanio	200	241	6.9	421	2	09EPN6_HENCA	09epn6 heterocepha
128	269.5	7.7	280	2	08C4R9_MOUSE	08c4r9 mus musculu	201	241	6.9	421	2	02MDJ5_9RODE	02mdj5 elurus sp.
129	269	7.7	343	2	05N0J6_BRARE	05njj6 brachydanio	202	240.5	6.9	344	2	07Y0X2_MONDO	07y0x2 monodelphis
130	269	7.7	434	2	05N0J8_BRARE	05njj8 brachydanio	203	240.5	6.9	344	2	07Y0Y4_CAERU	07y0y4 caenolestes
131	269	7.7	478	2	05N1W0_BRARE	05niw0 brachydanio	204	240.5	6.9	407	2	095KJ3_CABUN	095kj3 cabassous u
132	269	7.7	548	2	061H17_CAEBR	061h17 caenorhabdi	205	240.5	6.9	409	2	07YRS7_MICMU	07yrs7 micromys m
133	268.5	7.7	633	2	03TNZ7_MOUSE	03tnz7 mus musculu	206	240	6.9	421	2	09EPB4_9HYST	09epb4 capromys pi
134	268	7.7	460	2	05N0K1_BRARE	05nkj1 brachydanio	207	239.5	6.8	383	2	05GN63_9HYST	05gn63 echinmys did
135	266.5	7.6	810	2	08C435_MOUSE	08c435 mus musculu	208	239.5	6.8	385	2	091Y46_9RODE	091y46 steatomys s
136	266	7.6	2813	1	VWF_HUMAN	P04275 homo sapien	209	239.5	6.8	409	2	07YRS9_DADMA	07yrs9 daubentonla
137	264.5	7.6	320	2	04S337_TETNG	04s337 tetraodon n	210	239.5	6.8	414	2	097926_OCHPR	097926 ochotona pr
138	263	7.5	421	2	09EPD0_EREDO	09epd0 eethizon d	211	239	6.8	411	2	09XS43_PHYCA	09xs43 physeter ca
139	262.5	7.5	427	2	04RZK1_TETNG	04rzk1 tetraodon n	212	238.5	6.8	344	2	07Y0X5_PERRU	07y0x5 peromyscus
140	262	7.5	481	1	MATN3_MOUSE	035701 mus musculu	213	238.5	6.8	372	2	028449_TOXAF	028449 toxodonta a
141	262	7.5	481	2	054302_MOUSE	054302 mus musculu	214	238.5	6.8	413	2	08HXU4_EUPSX	08hxu4 euphractus
142	261.5	7.5	451	2	08N2G3_HUMAN	08n2g3 homo sapien	215	238	6.8	411	2	095KJ2_DASNO	095kj2 dasypus nov
143	259	7.4	409	2	02MDK9_HAPSI	02mdk9 haplaemur s	216	237.5	6.8	390	2	05GN62_9HYST	05gn62 echymus mac
144	258	7.4	385	2	091YG6_9RODE	091yg6 dactylops m	217	237.5	6.8	413	2	07YRS3_CALJA	07yrs3 callithrix
145	258	7.4	481	2	061R12_MOUSE	061r12 mus musculu	218	237.5	6.8	414	2	02MDL8_BRAAL	02mdl8 brachyctaro
146	257	7.3	420	2	02MDK7_9RODE	02mdk7 hyogeomys	219	237.5	6.8	415	2	097924_GLACO	097924 lepus craws
147	256.5	7.3	344	2	07Y0K7_PHAOR	07y0k7 phalangier o	220	236.5	6.8	417	2	09Z0R1_CAVPO	09z0r1 cavia porce
148	256.5	7.3	443	2	04T9U6_TETNG	04t9u6 tetraodon n	221	236	6.7	385	2	091Y47_9RODE	091y47 sicista kaz
149	253.5	7.2	427	2	028352_DUGDU	028352 dugong dugo	222	236	6.7	385	2	091YC1_9RODE	091yc1 phodopus ro
150	252.5	7.2	1019	1	CO6A1_CHICK	P07085 gallus gall	223	236	6.7	416	2	09Z0U7_MYOOL	09z0u7 myoxos glis
151	252	7.2	411	2	0284U0_ELEMA	0284u0 elephas max	224	235.5	6.7	383	2	05GN66_9HYST	05gn66 isochrix bi
152	251.5	7.2	1816	1	06N1T5_BRARE	06n1t5 brachydanio	225	235.5	6.7	386	2	091YC3_9MURI	091yc3 otomys ango
153	251	7.2	486	2	MATN3_HUMAN	015232 homo sapien	226	235.5	6.7	411	2	09X5A2_ESCGI	09x5a2 eschrichticu
154	251	7.2	486	2	04ZG02_HUMAN	04zgo2 homo sapien	227	235.5	6.7	411	2	09EPJ5_9HYST	09epj5 proechimys
155	250	7.1	409	2	09Z0O8_DIPSA	09z0o8 dipus sagitt	228	235	6.7	416	2	09Z0N6_9HYST	09z0n6 trichys fas
156	249	7.1	409	2	02MDL4_EULFU	02mdl4 eullemur ful	229	234.5	6.7	390	2	05GN60_9HYST	05gn60 echymus bla
157	249	7.1	751	2	03UWS2_MOUSE	03uws2 mus musculu	230	234.5	6.7	410	2	09TT41_PTEHP	09tt41 peromyscus hy
158	248.5	7.1	452	2	018936_AMBHO	018936 amblysomus	231	234.5	6.7	411	2	09GL86_MEGNO	09gl86 megapteta n
159	248.5	7.1	452	2	MATN3_CHICK	042401 gallus gall	232	234.5	6.7	412	2	08MWS6_CROKS	08mws6 crocodura r
160	248.5	7.1	589	2	07ZX63_XENLA	07zx63 xenopus lae	233	234.5	6.7	772	2	061L29_CAEBR	061l29 caenorhabdi
161	248.5	7.1	2482	1	VWF_PIG	Q28833 sus scrofa	234	234	6.7	406	2	077672_SCAAQ	077672 scaplopus aq
162	248	7.1	230	2	04KTX1_CEREL	04ktx1 cervus elap	235	234	6.7	1144	2	05NKT4_PANTR	05nkt4 pan troglod
163	248	7.1	637	2	08IVX1_HUMAN	08ivx1 homo sapien	236	233.5	6.7	401	2	07YRS8_PROVE	07yrs8 propithecus
164	248	7.1	1284	2	04VX05_HUMAN	04vx05 homo sapien	237	233.5	6.7	410	2	08HXT6_ZABPI	08hxt6 zaeagymys pic
165	248	7.1	1284	1	06P159_HUMAN	06p159 homo sapien	238	233.5	6.7	413	2	02MDL0_GALFA	02mdl0 galidictis b
166	248	7.1	1329	1	COXAI_HUMAN	09p218 homo sapien	239	233.5	6.7	414	2	09EPB2_9HYST	09epb2 diomys bta
167	247.5	7.1	344	2	07Y0Y3_CALPD	07y0y3 caluromys p	240	233.5	6.7	415	2	02MDK3_9EUTH	02mdk3 setifer set
168	247	7.1	385	2	091YH1_CRIMI	091yh1 cricetulus	241	233.5	6.7	1071	2	04SNW1_TETNG	04snw1 tetraodon n
169	246.5	7.0	375	2	09BGW7_DIDMA	09bgw7 didelphis m	242	233	6.7	410	2	08MWS3_NASTP	08mws3 natalus str
170	246.5	7.0	407	2	09TV41_ATEBE	09tv41 ateles belz	243	233	6.7	412	2	08HXT9_TOJMA	08hxt9 tolpeutes
171	246	7.0	430	1	VWF_RAT	062293 rattus norv	244	233	6.7	416	2	09UKT2_9HYST	09ukt2 bathyergus
172	245.5	7.0	405	2	095KU6_CYCDI	095ku6 cyclops di	245	233	6.7	421	2	09EPB6_AGOPA	09epb6 agouti paca
173	245.5	7.0	414	2	07YRS5_CEBAP	07yrs5 cebus apelli	246	232.5	6.6	385	2	091YK2_PERMA	091yk2 peromyscus
174	245	7.0	410	2	09Z0O6_GLAVO	09z0o6 glaucomys v	247	232	6.6	385	2	091YK6_9RODE	091yk6 myopialax s
175	245	7.0	416	2	07YRTO_LEMCA	07yrt0 lemur catla	248	232	6.6	409	2	028549_ORYAF	028549 orycteropus
176	245	7.0	421	2	09EPB1_9HYST	09epb1 echinys chr	249	232	6.6	411	2	08K1M0_JANOSF	08k1m0 anomalurus
177	244.5	7.0	411	2	08K1I9_CASCN	08k1i9 castor cana	250	232	6.6	417	2	09Z0O9_DRYNI	09z0o9 dryomys nlt

251	232	6.6	421	2	Q9PPE_9HYST	Q9PPE_clethronom	324	221	6.3	407	2	Q28357_DOBMO	Q28357_dobsonia mo
252	231.5	6.6	390	2	Q5GN8_9HYST	Q5GN8_titonomys pa	325	221	6.3	920	2	Q28984_PIG	Q28984_sus scrofa
253	231.5	6.6	402	2	Q9TSP0_PROPH	Q9TSP0_procoenoid	326	220.5	6.3	357	2	Q60YEL_CABER	Q60YEL_caenorhabdi
254	231.5	6.6	409	2	Q77671_ECHTE	Q77671_echinops te	327	220.5	6.3	385	2	Q5GN6_9HYST	Q5GN6_titonomys yo
255	231	6.6	385	2	Q91YF7_9RODE	Q91YF7_macroctarom	328	220.5	6.3	385	2	Q91YH3_CRIGA	Q91YH3_cricetomys
256	231	6.6	385	2	Q91YH2_CLEGL	Q91YH2_clethronom	329	220.5	6.3	395	2	Q77673_CHAVI	Q77673_chaetoptnac
257	231	6.6	387	2	Q8HXU1_PRIMA	Q8HXU1_pricodontes	330	220.5	6.3	403	2	Q9MZE8_DELE	Q9MZE8_delpinapte
258	231	6.6	410	2	Q92114_9RODE	Q92114_allactaga e	331	220.5	6.3	411	2	Q9EPJ4_9HYST	Q9EPJ4_petromus ty
259	231	6.6	421	2	Q9E0S2_AARBE	Q9E0S2_abrococa be	332	220.5	6.3	415	2	Q2MDK4_9HYST	Q2MDK4_craeonycte
260	231	6.6	1152	1	ITAM_HUMAN	P11215 homo sapien	333	220	6.3	385	2	Q91YAS_TATGH	Q91YAS_taterata kemp
261	231	6.6	1152	2	Q4VAKO_HUMAN	Q4VAKO homo sapien	334	220	6.3	385	2	Q91YGA_9RODE	Q91YGA_gerbillus h
262	231	6.6	1152	2	Q4VAK1_HUMAN	Q4VAK1 homo sapien	335	220	6.3	385	2	Q91YH0_9RODE	Q91YH0_caliomyscus
263	231	6.6	1152	2	Q4VAK2_HUMAN	Q4VAK2 homo sapien	336	220	6.3	409	2	Q9TSP7_GALCR	Q9TSP7_galago cras
264	230.5	6.6	413	2	Q2MDK5_9EUTH	Q2MDK5_limnogale m	337	219.5	6.3	391	2	Q5GN67_9HYST	Q5GN67_dactylomys
265	229.5	6.6	383	2	Q5GN5_9HYST	Q5GN5_trichomys h	338	219.5	6.3	408	2	Q7YRM5_9EUTH	Q7YRM5_elephantulu
266	229.5	6.6	402	2	Q8WN27_NYCAL	Q8WN27_nyctilimene a	339	219.5	6.3	421	2	Q9JIK8_MASWZ	Q9JIK8_mascoutiera
267	229.5	6.6	414	2	Q2MDL1_GALLEE	Q2MDL1_gallidia ele	340	219.5	6.3	1162	1	ITAD_HUMAN	Q13339 homo sapien
268	229	6.5	365	2	Q64216_9RODE	Q64216_galaxa zemm	341	219.5	6.3	1177	2	Q59H14_HUMAN	Q59H14_homo sapien
269	229	6.5	385	2	Q91YGS_9RODE	Q91YGS_dicrostomys	342	219	6.2	393	2	Q5G5W2_CRATH	Q5G5W2_craeonycte
270	229	6.5	421	2	Q9EPPE_9HYST	Q9EPPE_cryptomys h	343	218.5	6.2	382	2	Q91YG3_JACJA	Q91YG3_jaculus jac
271	229	6.5	572	2	Q21540_CABEL	Q21540_caenorhabdi	344	218.5	6.2	393	2	Q9GL87_MESPE	Q9GL87_mesopodon
272	229	6.5	967	2	Q3UIW4_MOUSE	Q3UIW4 mus musculu	345	218	6.2	396	2	Q6JC71_9EUTH	Q6JC71_solenodon p
273	229	6.5	1064	2	Q3TBT0_MOUSE	Q3TBT0 mus musculu	346	218	6.2	398	2	Q9TSU5_PELCA	Q9TSU5_felis silve
274	229	6.5	1153	1	ITAM_MOUSE	P05555 mus musculu	347	218	6.2	403	2	Q8WN32_NOCHL	Q8WN32_noctilio al
275	229	6.5	1153	2	Q3TD86_MOUSE	Q3TD86 mus musculu	348	218	6.2	414	2	Q2MDL2_FOSFO	Q2MDL2_fossa fossa
276	229	6.5	1153	2	Q3U415_MOUSE	Q3U415 mus musculu	349	217.5	6.2	365	2	Q8WN37_ROUMM	Q8WN37_rousetus a
277	229	6.5	1166	2	Q3UJF0_MOUSE	Q3UJF0 mus musculu	350	216	6.2	385	2	Q91YCA_9RODE	Q91YCA_nesomys ruf
278	229	6.5	1232	2	Q3UIU4_MOUSE	Q3UIU4 mus musculu	351	215.5	6.2	383	2	Q5GN61_9HYST	Q5GN61_proechinys
279	228.5	6.5	391	2	Q5GN69_MESHI	Q5GN69_mesomys his	352	215.5	6.2	410	2	Q8MI57_PLENU	Q8MI57_plecticus au
280	228.5	6.5	414	2	Q2MDK6_CRYPE	Q2MDK6_cryptoproc	353	215.5	6.2	421	2	Q2MDK1_VIVIN	Q2MDK1_viverricula
281	228.5	6.5	421	2	Q9UK21_CHITLA	Q9UK21_chinchilla	354	214.5	6.1	2401	2	Q7RF52_PLAYO	Q7RF52_furpterus
282	228.5	6.5	789	2	Q9BKQ4_CABEL	Q9BKQ4_caenorhabdi	355	214	6.1	399	2	Q5G5W4_FURHO	Q5G5W4_furpterus
283	228	6.5	417	2	Q920R2_9HYST	Q920R2_sphigxurus	356	214	6.1	409	2	Q5KUP5_CHODI	Q5KUP5_choloepus d
284	228	6.5	410	2	Q920Q3_MARMO	Q920Q3_marmota mon	357	214	6.1	1169	2	Q3UIP9_MOUSE	Q3UIP9_mus musculu
285	228	6.5	1028	1	Q6GAI_HUMAN	P12109 homo sapien	358	213.5	6.1	411	2	Q9JIK7_PEDCA	Q9JIK7_pedetes cap
286	228	6.5	1163	1	ITAX_HUMAN	P72645 homo sapien	359	213.5	6.1	1169	2	Q28904_PIG	Q28904_sus scrofa
287	228	6.5	1163	2	Q9GL88_HINIG	P20702 homo sapien	360	213.5	6.1	1286	2	Q9TXR6_CABEL	Q9TXR6_caenorhabdi
288	227.5	6.5	411	2	Q9BSA8_HUMAN	Q9BSA8_homo sapien	361	213	6.1	2255	2	Q4SD21_TETNG	Q4SD21_tetraodon n
289	227.5	6.5	421	2	Q9EPN7_HELAR	Q9EPN7_heliophobu	362	212.5	6.1	390	2	Q7YR18_PTBP	Q7YR18_pteronodon
290	227	6.5	421	2	Q9JIK20_9HYST	Q9JIK20_octodon lun	363	212.5	6.1	406	2	Q8WN26_DESKO	Q8WN26_desmodus ro
291	227	6.5	421	2	Q2MDK2_SURSU	Q2MDK2_suricata su	364	212.5	6.1	1161	1	ITAD_RAT	Q9JIK7_rattus norv
292	226.5	6.5	413	2	Q28349_CYNVA	Q28349_cynocephalu	365	212	6.1	358	2	Q9TV39_TUPEL	Q9TV39_tupia glis
293	226.5	6.5	427	2	Q8TBZ2_HUMAN	Q8TBZ2_homo sapien	366	212	6.1	365	2	Q9XSA4_IAMGL	Q9XSA4_lama glama
294	226.5	6.5	439	2	Q6GAI_MOUSE	Q6GAI_mus musculu	367	212	6.1	410	2	Q19029_9EUTH	Q19029_mantis sp. v
295	226.5	6.5	1025	1	Q5GN57_9HYST	Q5GN57_titonomys se	368	212	6.1	430	2	Q8MI60_TADIN	Q8MI60_taderrida in
296	225.5	6.4	408	2	Q7YRP9_NYCCO	Q7YRP9_nycticebus	369	212	6.1	423	2	Q8MI14_BRATR	Q8MI14_bradypus tr
297	225.5	6.4	414	2	Q2MDJ3_9CARN	Q2MDJ3_eupleres go	370	212	6.1	1169	1	ITAX_MOUSE	Q9JIK4_mus musculu
298	225	6.4	387	2	Q5SKQ4_TAMTE	Q5SKQ4_tamandua te	371	212	6.0	200	2	Q88494_MOUSE	Q88494_mus musculu
300	225	6.4	391	2	Q5GN55_9HYST	Q5GN55_euryzygomat	372	211.5	6.0	323	2	Q7YXQ9_NORTY	Q7YXQ9_notoctyes
301	225	6.4	399	2	Q2MDK6_LEPED	Q2MDK6_lepitemur e	373	211.5	6.0	410	2	Q8MI53_EPTNI	Q8MI53_pesticus n
302	225	6.4	417	2	Q9Z0NS_THRSW	Q9Z0NS_thryonomys	374	211.5	6.0	410	2	Q8MI58_9CHIR	Q8MI58_barbaestella
303	224.5	6.4	421	2	Q2MDL7_CROCR	Q2MDL7_crocota cro	375	211.5	6.0	639	1	COCA1_EABIT	Q28902_cryptocolegus
304	224.5	6.4	1060	2	Q4SQQ3_TETNG	Q4SQQ3_tetraodon n	376	211	6.0	410	2	Q8MI59_9CHIR	Q8MI59_minicolegus
305	224	6.4	387	2	Q9SKS9_MYRTR	Q9SKS9_myrmecophag	377	211	6.0	1188	2	Q6KAS4_MOUSE	Q6KAS4_mus musculu
306	224	6.4	412	2	Q8HXW8_TALEU	Q8HXW8_talpa europ	378	210.5	6.0	385	2	Q91YVA_9RODE	Q91YVA_tachyorycte
307	223.5	6.4	368	2	Q28364_EQUAS	Q28364_equus asinu	379	210.5	6.0	389	2	Q8WN35_9CHIR	Q8WN35_nyctereis gr
308	223	6.4	411	2	Q9EPJ7_ATHMA	Q9EPJ7_atherurus m	380	210.5	6.0	410	2	Q8MI50_9CHIR	Q8MI50_murina ussu
309	223	6.4	383	2	Q9MZE6_ZIPCA	Q9MZE6_ziphius cav	381	210.5	6.0	862	2	Q615W4_CABER	Q615W4_caenorhabdi
310	222.5	6.4	383	2	Q5GN54_9HYST	Q5GN54_proechinys	382	210.5	6.0	2098	2	Q25757_PLAFA	Q25757_plasmiodum
311	222.5	6.4	383	2	Q5GN68_9HYST	Q5GN68_olymys lat	383	210	6.0	397	2	Q5GN64_9HYST	Q5GN64_kannabateom
312	222.5	6.4	407	2	Q7YRM3_MACPR	Q7YRM3_macroscecid	384	210	6.0	421	2	Q7YR17_MYSTU	Q7YR17_myscactia t
313	222.5	6.4	408	2	Q7YRM6_PETTE	Q7YRM6_petridromus	385	210	6.0	421	2	Q9JIK19_CTEVA	Q9JIK19_tetradactyla
314	222.5	6.4	1268	2	Q616M0_CABER	Q616M0_caenorhabdi	386	209.5	6.0	467	2	Q4RBL7_TETNG	Q4RBL7_tetraodon n
315	222	6.3	350	2	Q5GN65_9HYST	Q5GN65_isothrix si	387	209.5	6.0	1022	1	COE62_CHICK	Q91Y48_gallus galli
316	222	6.3	365	2	Q8KNZ9_ROUMM	Q8KNZ9_rousetus a	388	209.5	6.0	385	2	Q920J8_ACOCA	Q920J8_aconys cahl
317	222	6.3	385	2	Q8HXU7_DASKA	Q8HXU7_dasyopus kap	389	208.5	6.0	410	2	Q8MI56_9CHIR	Q8MI56_scothophilus
318	222	6.3	410	2	Q8WN30_9CHIR	Q8WN30_himolophus	390	208	5.9	2957	2	Q4REVB_TETNG	Q4REVB_tetraodon n
319	222	6.3	410	2	Q9T40_HIPCO	Q9T40_hipposidero	391	207.5	5.9	410	2	Q8MI52_VESSU	Q8MI52_vesperfiliu
320	222	6.3	1125	2	Q2UYO9_HUMAN	Q2UYO9_homo sapien	392	207.5	5.9	1170	1	ITAX_HUMAN	Q20701_homo sapien
321	221.5	6.3	385	2	Q91YR8_MESAV	Q91YR8_mesocricetu	393	207.5	5.9	1170	2	Q5NK16_PANTR	Q5NK16_pan troglod
322	221.5	6.3	405	2	Q7YRM8_9EUTH	Q7YRM8_elephantulu	394	207	5.9	410	2	Q9T443_MOVE	Q9T443_myotis vell
323	221	6.3	385	2	Q91YCS_NEOFU	Q91YCS_neotoma fus	395	207	5.9	960	2	Q4RSP3_TETNG	Q4RSP3_tetraodon n

397	206.5	5.9	146	2	05TF09_HUMAN	05tfo9 homo sapien	470	188.5	5.4	1171	2	042094_CHICK	042094 gallus gall
398	206.5	5.9	391	2	08WN28_NYCTH	08wn28 nycteris th	471	188.5	5.4	1620	2	08IK83_PLAF7	08ik83 plasmodium
399	206	5.9	410	2	08M151_MYOVA	08m151 myotis yarb	472	187.5	5.4	1170	1	ITR2_BOVIN	P53173 bos taurus
400	205.5	5.9	382	2	091VG7_9RODE	091vg7 deomys ferr	473	187.5	5.4	1188	1	ITR11_MOUSE	P61622 mus musculu
401	205	5.9	979	2	08N471_HUMAN	08n471 homo sapien	474	187	5.3	146	2	04KTM5_CEREL	04ktm5 cerus elap
402	205	5.9	1029	1	CO6A2_MOUSE	002788 mus musculu	475	187	5.3	1197	2	04UBP9_THEAN	04ubp9 thelleria a
403	205	5.9	1034	2	08K229_MOUSE	08k229 mus musculu	476	186	5.3	1070	2	04N1E8_THEPA	04n1e8 thelleria p
404	204.5	5.8	831	2	04Y774_PLACH	04y774 plasmodium	477	185	5.3	269	2	08OWE9_RAT	08owe9 rattus norv
405	204	5.8	343	2	08WN34_ANTPA	08wn34 antrozous p	478	184.5	5.3	322	2	07YXO0_TETNG	07yxo0 petaurus br
406	204	5.8	369	2	029128_9CHIR	029128 conatia sau	479	184.5	5.3	565	2	04SOR9_TETNG	04sor9 tetraodon n
407	204	5.8	13100	2	009165_CAEEL	009165 caenorhabdi	480	184.5	5.3	643	2	018290_CAEEL	018290 caenorhabdi
408	203.5	5.8	405	2	09T142_EMBAT	09t142 emballonura	481	184.5	5.3	845	2	05VTE5_HUMAN	05vte5 homo sapien
409	203.5	5.8	410	2	08M154_PIPAB	08m154 pipistrellu	482	184.5	5.3	3548	2	05VTE4_HUMAN	05vte4 homo sapien
410	203.5	5.8	2114	1	ITR1_RAT	P18614 rattus norv	483	184.5	5.3	3574	2	04LDE5_HUMAN	04lde5 homo sapien
411	203.5	5.8	11019	2	097267_PLAF7	097267 plasmodium	484	184	5.3	318	2	028341_CYNBP	028341 cynopterus
412	203	5.8	1019	2	06P001_HUMAN	06p001 homo sapien	485	184	5.3	445	2	06PCB0_HUMAN	06pcb0 homo sapien
413	202.5	5.8	322	2	07YXO0_DROAU	07yxo0 dromiciops	486	183.5	5.2	314	2	07YXO3_DASAL	07yxo3 dasyrus al
414	202.5	5.8	1332	2	09BP08_HALRO	09bp08 halocynthia	487	183.5	5.2	319	2	03URV2_MOUSE	03urv2 mus musculu
415	202	5.8	139	2	04RV00_TETNG	04rv10 tetraodon n	488	183.5	5.2	1165	1	ITR1L_BOVIN	P61625 bos taurus
416	202	5.8	403	2	028410_FELCA	028410 felis silve	489	183.5	5.2	1354	2	06TYB8_BOVIN	06tyb8 bos taurus
417	202	5.8	1141	2	02UY11_MOUSE	02uy11 mus musculu	490	183	5.2	354	2	016003_HYDAT	016003 hydra atten
418	201.5	5.8	1166	2	05RL93_BRARE	05rl93 brachydanio	491	182.5	5.2	440	2	08CBT2_MOUSE	08cbt2 mus musculu
419	200.5	5.7	406	2	091W4_MOUSE	099144 mus musculu	492	182.5	5.2	848	2	08C720_MOUSE	08c720 mus musculu
420	200	5.7	385	2	091Y61_PRODE	091y61 lophuromys	493	182.5	5.2	1181	1	ITR2_HUMAN	P17301 homo sapien
421	200	5.7	425	2	09B0M6_HUMAN	09b0m6 homo sapien	494	182.5	5.2	3567	2	09ES77_MOUSE	09es77 mus musculu
422	200	5.7	1014	2	05FWW2_XENLA	05fww2 xenopus lae	495	181.5	5.2	415	2	0642A6_RAT	0642a6 rattus norv
423	200	5.7	1019	1	CO6A2_HUMAN	P12110 homo sapien	496	181.5	5.2	362	2	07YXO2_ECHKA	07yxo2 echymipera
424	199.5	5.7	334	2	07YRM4_ELEED	07yrm4 elephanthu	497	181	5.2	363	2	04SNW2_TETNG	04snw2 tetraodon n
425	199.5	5.7	410	2	08WN33_9CHIR	08wn33 rhogeessa t	498	180.5	5.2	1349	2	04TBJ2_TETNG	04tbj2 tetraodon n
426	199.5	5.7	505	2	04SCD1_TETNG	04scd1 tetraodon n	499	179.5	5.1	326	2	08HXM7_GALPY	08hxm7 galenys pyr
427	199	5.7	407	2	07YRS6_TARBA	07yrs6 taraius ban	500	179	5.1	1196	2	098TF1_CYPCA	098tf1 cyprius ca
428	198.5	5.7	369	2	028340_CERSI	028340 ceratotheri	501	179	5.1	1395	2	04XZL5_PLACH	04xzl5 plasmodium
429	198.5	5.7	369	2	028405_ELEUR	028405 elephanthu	502	178	5.1	763	2	031430_LAMJA	031430 lamapetra ja
430	198.5	5.7	682	2	03V391_MOUSE	03v391 mus musculu	503	177	5.1	422	2	08K118_DIPME	08k118 dipodomys m
431	198.5	5.7	1179	2	03V3R4_MOUSE	03v3r4 mus musculu	504	177	5.1	1009	2	04SNW2_TETNG	04snw2 tetraodon n
432	198	5.7	406	2	028492_MEGIL	028492 megaderma t	505	177	5.1	1614	2	04ZOF4_PLABE	04zof4 plasmodium
433	197.5	5.6	322	2	07YQX8_SWETA	07yqx8 pseudochiro	506	176	5.0	1547	2	07RD70_PLAYO	07rd70 plasmodium
434	197.5	5.6	410	2	08M155_9CHIR	08m155 nyctalus av	507	175.5	5.0	1187	2	098TF0_CYPCA	098tf0 cyprius ca
435	196.5	5.6	415	2	08R225_MOUSE	08r225 mus musculu	508	175	5.0	310	2	09MZ67_GLOMA	09mz67 globicephal
436	196.5	5.6	415	2	0923K3_MOUSE	0923k3 mus musculu	509	174.5	5.0	1016	2	061WN4_CAEER	061wn4 caenorhabdi
437	196.5	5.6	1042	2	04RIX3_TETNG	04rix3 tetraodon n	510	173.5	5.0	418	2	03YV22_BIOGL	03yv22 biopharlari
438	195	5.6	752	2	04ROP0_TETNG	04rop0 tetraodon n	511	173	4.9	682	2	07YXK2_BOVIN	07yxk2 bos taurus
439	195	5.6	1160	2	09R200_MOUSE	09r200 mus musculu	512	172.5	4.9	364	2	019013_ERIEU	019013 elimphaeus e
440	195	5.6	1161	2	03T9N8_MOUSE	03t9n8 mus musculu	513	172.5	4.9	418	2	03YXV1_BIOGL	03yv11 biopharlari
441	195	5.6	1161	2	03T8B5_MOUSE	03t8b5 m b6-derive	514	172.5	4.9	565	2	06ZW26_HUMAN	06zw26 homo sapien
442	195	5.6	1161	2	09WTV4_MOUSE	09wtv4 mus musculu	515	172.5	4.9	689	2	001545_CAEEL	001545 caenorhabdi
443	195	5.6	1162	2	03U159_MOUSE	03u159 mus musculu	516	172	4.9	336	2	05G5W7_ARTJA	05g5w7 artibeus ja
444	195	5.6	1163	1	ITR1L_MOUSE	P24063 mus musculu	517	171.5	4.9	1202	2	03U171_MOUSE	03u171 mus musculu
445	194	5.5	385	2	091YV3_URARU	091yv3 uranomys ru	518	171.5	4.9	1313	2	071A42_CAEER	071a42 caenorhabdi
446	193.5	5.5	395	2	08HXM9_9EUTH	08hxm9 biarinella	519	171	4.9	712	2	043981_EIMTE	043981 eimeria ten
447	193.5	5.5	1172	2	03OK17_PIG	03ok17 sus scrofa	520	170.5	4.9	1045	2	0801S8_XENLA	0801s8 xenopus lae
448	193.5	5.5	1173	2	03OK18_PIG	03ok18 sus scrofa	521	170.5	4.9	615	2	060X10_CAEER	060x10 caenorhabdi
449	193	5.5	422	2	08K116_THOTA	08k116 thomomys ta	522	170.5	4.9	1178	1	ITR2_MOUSE	062469 mus musculu
450	193	5.5	1151	1	ITR1L_HUMAN	P56199 homo sapien	523	170.5	4.9	1178	2	06PIC7_MOUSE	06pic7 mus musculu
451	192.5	5.5	415	2	08C0O7_MOUSE	08c0o7 mus musculu	524	170	4.9	311	2	08MN36_9CHIR	08mn36 tapozorus b
452	192.5	5.5	1168	1	ITR4D_MOUSE	Q3V0C4 mus musculu	525	169	4.8	725	2	07YXK1_BOVIN	07yxk1 bos taurus
453	192.5	5.5	1189	1	ITR1L_HUMAN	Cuukx5 homo sapien	526	168	4.8	202	2	04T1H8_TETNG	04t1h8 tetraodon n
454	192	5.5	108	2	04TER3_TETNG	Q4tec3 tetraodon n	527	167.5	4.8	304	2	06P666_MOUSE	06p666 mus musculu
455	192	5.5	1164	2	04QWZ3_SHEEP	Q4qwx3 ovis aries	528	167.5	4.8	323	2	08CBR4_MOUSE	08cbt4 microptero
456	192	5.5	1165	2	04QWZ2_SHEEP	Q4qwx2 ovis aries	529	167.5	4.8	324	2	08S017_MICLA	08s017 thelleria p
457	191.5	5.5	599	2	08WVQ1_PASCI	Q8wvq1 bolentia vi	530	167.5	4.8	552	2	04N2P2_THEPA	04n2p2 thelleria p
458	191.5	5.5	1188	2	07TQC3_MOUSE	Q7tqc3 mus musculu	531	167.5	4.8	1167	1	ITR2E_MOUSE	060677 mus musculu
459	191	5.5	329	2	07YRM7_ELEMY	Q7yrm7 elephanthu	532	167	4.8	630	2	029124_PIG	029124 caenorhabdi
460	191	5.5	403	2	05G5W5_THYTR	05g5w5 thrioptera	533	166.5	4.8	191	2	061JN2_CAEER	061jn2 caenorhabdi
461	190.5	5.4	205	2	063001_RAT	063001 rattus norv	534	166.5	4.8	319	2	08HXM6_9EUTH	08hxm6 uropisles s
462	190.5	5.4	833	2	096442_STRPU	096442 strongyloce	535	166.5	4.8	487	2	09HOB8_HUMAN	09hob8 homo sapien
463	190	5.4	411	2	09XSA1_HIPAM	Q9xsa1 hippopotamu	536	166.5	4.8	889	2	05GCC1_CARKO	05gcc1 carinascor
464	190	5.4	1164	2	032Y14_CAPIH	Q32y14 capra hircu	537	166.5	4.8	1160	2	08MKF4_FELCA	08mkf4 felis silve
465	190	5.4	1165	2	032Y13_CAPIH	Q32y13 capra hircu	538	166	4.7	314	2	05G5W6_ANOGE	05g5w6 anoura geof
466	189.5	5.4	1905	2	09XTP6_PLABE	Q9xtp6 plasmodium	539	166	4.7	394	2	08IRG8_BIOGL	08irg8 biopharlari
467	189	5.4	1160	2	03T1I6_RAT	Q3t1i6 rattus norv	540	165.5	4.7	1038	2	08BSO1_MOUSE	08bs01 mus musculu
468	188.5	5.4	285	1	ITR1L_CHICK	Q90615 gallus gall	541	165.5	4.7	1167	2	05SRV0_MOUSE	05srv0 mus musculu
469	188.5	5.4	322	2	07YXK1_SWETA	Q7yqx1 rhycholest	542	165	4.7	333	2	05G5W3_EUMAN	05g5w3 eunops auri

543	165	4.7	1031	2	Q4SHJ3_TETNG	Q4shj3 tetraodon n	616	139	4.0	676	2	Q5F3F4_CHICK	Q5f3f4 gallus galli
544	165	4.7	1247	2	Q5CLRE_CRYHO	Q5clre cryptospori	617	138.5	4.0	747	2	Q6NM57_BRARE	Q6nm57 brachydanio
545	165	4.7	1247	2	Q5CU06_CRYPV	Q5cu06 cryptospori	618	138	3.9	436	2	Q95L15_MACFA	Q95l15 macaca fasc
546	164.5	4.7	633	2	Q4SVDF_TETNG	Q4svdf tetraodon n	619	138	3.9	923	2	Q5AUS9_EMENT	Q5aus9 emmentillus
547	164.5	4.7	895	2	Q9WUP8_9MURI	Q9wup8 mus sp. itg	620	137.5	3.9	406	2	Q9TV40_TRADR	Q9tv40 tadaria br
548	164.5	4.7	1166	2	Q3U4V9_MOUSE	Q3u4v9 mus musculu	621	137	3.9	744	2	Q5SK30_CRYNE	Q5sk30 cryptococcu
549	163.5	4.7	1167	2	Q08J40_RAT	Q08j40 rattus norv	622	136.5	3.9	1601	2	Q4UEZ8_THEAN	Q4uez8 thelleria a
550	163.5	4.7	765	2	Q9U8J9_NEOCA	Q9u8j9 neospora ca	623	136	3.9	1779	2	Q6IX39_CAEHR	Q6ix39 caenorhabdi
551	163.5	4.7	1250	2	Q3S621_TOXGO	Q3s621 toxoplasma	624	135.5	3.9	577	2	Q5GZ84_XANOR	Q5gz84 xenothoma s
552	163	4.6	1086	2	Q96HB1_HUMAN	Q96hb1 homo sapien	625	135.5	3.9	833	2	Q8YUR6_XANSP	Q8yur6 arabomasa sp
553	162.5	4.6	497	2	Q6UMHO_HUMAN	Q6umho homo sapien	626	135	3.9	1234	2	Q4YBD6_PLACH	Q4ybd6 plasmodium
554	162.5	4.6	1179	1	ITAE_HUMAN	ITAE_HUMAN	627	135	3.9	1304	2	Q8WTE3_PLABE	Q8wte3 plasmodium
555	161.5	4.6	305	2	Q7YQX4_9META	Q7yqx4 smnthopis	628	134.5	3.8	403	2	Q7SY04_BRARE	Q7sy04 brachydanio
556	160.5	4.6	1167	2	Q08J41_RAT	Q08j41 rattus norv	629	134	3.8	921	2	Q921U8_MOUSE	Q921u8 mus musculu
557	160	4.6	473	2	Q4SMW7_TETNG	Q4smw7 tetraodon n	630	134	3.8	1246	2	Q3S622_TOXGO	Q3s622 toxoplasma
558	160	4.6	1083	2	Q2E423_CARRO	Q2e423 carciinoscor	631	134	3.8	12268	2	Q8M008_CAEHL	Q8m008 caenorhabdi
559	159.5	4.6	1019	1	LRC_CARRO	LRC_CARRO	632	133.5	3.8	577	2	Q2P294_XANOR	Q2p294 xanthomonas
560	159.5	4.6	1019	1	LRC_TACTR	LRC_TACTR	633	133.5	3.8	715	1	DCBD1_HUMAN	DCBD1_HUMAN
561	159.5	4.6	1019	1	Q8T9S1_TACTR	Q8t9s1 tachypneus	634	133	3.8	234	2	Q405F1_9RHOB	Q405f1 janiaschia
562	159	4.6	769	2	Q00816_TOXGO	Q00816 toxoplasma	635	133	3.8	683	2	Q2UA88_ASFOR	Q2ua88 aspergillus
563	159	4.5	1969	2	Q069H6_CIOIN	Q069h6 ciona intes	636	132.5	3.8	244	2	Q2VCM5_9CARN	Q2vcn5 vulpes cana
564	158.5	4.5	156	2	Q7IVJ3_HUMAN	Q7ivj3 homo sapien	637	132.5	3.8	921	2	Q8CD93_MOUSE	Q8cd93 mus musculu
565	157.5	4.5	293	2	Q7YQX5_PHATA	Q7yqx5 phascogale	638	132.5	3.8	1063	2	Q8WPR4_HUMAN	Q8wpr4 homo sapien
566	157.5	4.5	1451	2	Q5CNE9_CRYHO	Q5cne9 cryptospori	639	132.5	3.8	1063	2	Q8WPR4_HUMAN	Q8wpr4 homo sapien
567	157	4.5	516	2	Q5TDB6_HUMAN	Q5tdb6 homo sapien	640	132	3.8	1063	2	Q8WPR4_HUMAN	Q8wpr4 homo sapien
568	156.5	4.5	494	2	Q3U4C7_MOUSE	Q3u4c7 mus musculu	641	132	3.8	1247	2	Q817Z6_TOXGO	Q817z6 toxoplasma
569	156.5	4.5	494	2	Q9D2R3_MOUSE	Q9d2r3 m 10 day ol	642	131.5	3.8	241	2	Q99806_HUMAN	Q99806 homo sapien
570	156.5	4.5	495	2	Q08BQ2_MOUSE	Q08bq2 mus musculu	643	131.5	3.8	244	2	Q2VCL9_VITLZE	Q2vcl9 vulpes zerd
571	156	4.5	427	2	Q6ORL2_CAEHR	Q6orl2 caenorhabdi	644	131.5	3.8	244	2	Q2VCM0_VULVU	Q2vcn0 vulpes vulp
572	156	4.5	523	2	Q098ST_CHICK	Q098st gallus galli	645	131.5	3.8	244	2	Q2VCN1_9CARN	Q2vcn1 vulpes riep
573	155.5	4.4	1556	2	Q61139_CRYPV	Q61139 cryptospori	646	131.5	3.8	244	2	Q2VCM2_VULMA	Q2vcn2 vulpes macr
574	155	4.4	358	2	Q29134_TUPGL	Q29134 tupala gils	647	131.5	3.8	244	2	Q2VCM3_9CARN	Q2vcn3 vulpes cors
575	155	4.4	686	2	Q4WEG9_ASPFU	Q4weg9 aspergillus	648	131.5	3.8	244	2	Q2VCP8_ALOLA	Q2vcp8 aspergillus
576	155	4.4	1272	2	Q8IM24_PLAF7	Q8im24 plasmodium	649	131.5	3.8	328	2	Q3IEE7_PSEHT	Q3iee7 pseudoe lago
577	155	4.4	1674	2	Q5CZ08_CRYPV	Q5cz08 cryptospori	650	131.5	3.8	533	2	Q94677_PLACN	Q94677 plasmodium
578	154.5	4.4	425	2	Q6TIGR_CAEHR	Q6tigr caenorhabdi	651	131.5	3.8	572	2	Q9GSR0_PLACN	Q9gsr0 plasmodium
579	153.5	4.4	425	2	Q9GZFE_CAEHL	Q9gzfe caenorhabdi	652	131.5	3.8	713	2	Q6GL27_XENTR	Q6gl27 xenopus tro
580	153	4.4	393	2	Q4TUS0_NECAM	Q4tus0 necator ame	653	131	3.7	959	2	Q05504_MOUSE	Q05504 mus musculu
581	152	4.3	449	2	Q6P590_HUMAN	Q6p590 homo sapien	654	130.5	3.7	240	2	Q2VCM2_PSEGR	Q2vcn2 pseudalopec
582	152	4.3	500	2	Q4V9Y5_XENTR	Q4v9y5 xenopus tro	655	130.5	3.7	244	2	Q2VCM9_PSEVE	Q2vcn9 pseudalopec
583	151.5	4.3	1117	2	Q4RXN8_TETNG	Q4rxn8 tetraodon n	656	130.5	3.7	244	2	Q2VCM9_PSEVE	Q2vcn9 pseudalopec
584	151.5	4.3	1556	2	Q5CJ50_CRYHO	Q5cj50 cryptospori	657	130.5	3.7	713	2	Q6GN18_XENLA	Q6gn18 xenopus lae
585	150.5	4.3	724	2	Q04S88_ETWMA	Q04s88 etimera max	658	130	3.7	146	2	Q06930_PLAFA	Q06930 plasmodium
586	150.5	4.3	813	2	Q4XSS2_PLACH	Q4xss2 plasmodium	659	130	3.7	639	2	Q6K825_ORYSA	Q6k825 oryza sativ
587	149.5	4.3	784	2	Q2SVL5_BURTH	Q2svl5 burkholderi	660	129.5	3.7	244	2	Q2VCM6_9CARN	Q2vcn6 urocyon lit
588	149.5	4.3	1167	1	ITALIO_HUMAN	ITALIO_HUMAN	661	129.5	3.7	703	2	Q8N1Y7_NEUCR	Q8n1y7 neurospora
589	149	4.3	903	2	Q464T6_THEAN	Q464t6 thelleria a	662	129	3.7	482	2	Q8NA36_HUMAN	Q8na36 homo sapien
590	148	4.2	1615	2	Q7ROM4_PLAYO	Q7rom4 plasmodium	663	129	3.7	1251	2	Q4SQ95_TETNG	Q4sq95 tetraodon n
591	147.5	4.2	406	2	Q28638_GALCR	Q28638 galago cras	664	129	3.7	1784	2	Q9VE02_DROME	Q9ve02 drosophila
592	146.5	4.2	767	2	Q8KTM1_CLODI	Q8ktm1 clostridium	665	128.5	3.7	244	2	Q2VCM8_SPEVE	Q2vcn8 specheos ve
593	146.5	4.2	2359	2	Q4S0B4_TETNG	Q4s0b4 tetraodon n	666	128.5	3.7	244	2	Q2VCM9_PSEBU	Q2vcn9 pseudalopec
594	146	4.2	1304	2	Q4YUE0_PLABE	Q4yue0 plasmodium	667	128.5	3.7	244	2	Q2VCN1_PSEBY	Q2vcn1 pseudalopec
595	145	4.1	1613	2	Q4N5G4_THEPA	Q4n5g4 thelleria p	668	128.5	3.7	244	2	Q2VCN3_9CARN	Q2vcn3 pseudalopec
596	144.5	4.1	606	2	Q464T5_THEAN	Q464t5 thelleria a	669	128.5	3.7	244	2	Q2VCN9_CHRBR	Q2vcn9 chrysoecyon
597	143.5	4.1	171	2	Q8K018_MOUSE	Q8k018 mus musculu	670	128.5	3.7	244	2	Q2VCP7_ATEMT	Q2vcp7 atelocynus
598	143.5	4.1	500	2	Q9H336_HUMAN	Q9h336 homo sapien	671	128.5	3.7	244	2	Q2VCP7_ATEMT	Q2vcp7 atelocynus
599	143.5	4.1	767	2	Q8CGD2_MOUSE	Q8cgd2 m cocoacris	672	128.5	3.7	266	2	Q8C6V0_MOUSE	Q8c6v0 mus musculu
600	143.5	4.1	500	2	Q2N3V5_CLODI	Q2n3v5 clostridium	673	128.5	3.7	531	2	Q4V6F8_PLACH	Q4v6f8 plasmodium
601	143	4.1	931	2	Q4N102_THEPA	Q4n102 thelleria p	674	128.5	3.7	614	2	Q8VNU9_LACDL	Q8vnu9 lacobacilli
602	143	4.1	1530	2	Q7RP79_PLAYO	Q7rp79 plasmodium	675	128.5	3.7	845	2	Q8WUJ3_PLACH	Q8wuj3 plasmodium
603	142	4.1	106	2	Q4Y3E4_PLACH	Q4y3e4 plasmodium	676	128.5	3.7	921	2	Q9R0D0_MOUSE	Q9r0d0 mus musculu
604	142	4.1	655	2	Q6UJH3_BABBO	Q6ujh3 babesia bov	677	128.5	3.7	923	2	Q9R253_MOUSE	Q9r253 mus musculu
605	142	4.1	744	2	Q5KR99_CRYNE	Q5kr99 cryptococcu	678	128.5	3.7	1235	2	Q65979_CIOIN	Q65979 ciona intes
606	141.5	4.0	2938	2	Q61769_MOUSE	Q61769 mus musculu	679	128	3.7	909	2	Q2Z1I5_CALSA	Q2z1i5 caldicellul
607	141	4.0	371	2	Q96K61_HUMAN	Q96k61 homo sapien	680	128	3.7	1200	1	HYAL_STRPU	HYAL_STRPU
608	141	4.0	1562	2	Q5UWJ9_HALMA	Q5uwj9 haloarcula	681	127.5	3.6	244	2	Q2VCN5_OTOME	Q2vcn5 otocyon meg
609	140.5	4.0	429	2	Q7I6430_CAEHL	Q7i6430 caenorhabdi	682	127.5	3.6	429	2	Q6IRCS_CAEHR	Q6ircs caenorhabdi
610	140.5	4.0	449	2	Q7IUN8_CAEHL	Q7iun8 caenorhabdi	683	127.5	3.6	641	2	Q8BVW2_MOUSE	Q8bvwm2 mus musculu
611	140.5	4.0	921	2	Q3TCV2_MOUSE	Q3tcv2 mus musculu	684	127.5	3.6	1061	2	Q69YK7_HUMAN	Q69yk7 homo sapien
612	140	4.0	921	2	Q61PA3_CAEHR	Q61pa3 caenorhabdi	685	127.5	3.6	1103	2	Q9CAJ7_NEUCR	Q9caj7 neurospora
613	139.5	4.0	614	2	Q94674_PLAGA	Q94674 plasmodium	686	127.5	3.6	1837	2	Q9N5F6_CAEHL	Q9n5f6 caenorhabdi
614	139	4.0	503	1	DCBD1_MOUSE	DCBD1_MOUSE	687	127	3.6	419	1	RD23C_ARATH	RD23c arabidopsis
615	139	4.0	507	2	Q99MW6_MOUSE	Q99mwe mus musculu	688	127	3.6	1434	2	Q6NP25_DROME	Q6np25 drosophila

689	127	3.6	1766	2	Q2U7Y5_ASPOR	Q2u7y5 aspergillus	762	121.5	3.5	903	1	EC1C_BOVIN	P54281 bos taurus
690	127	3.6	1832	2	Q4PF70_USTMA	Q4pf70 ustilaago ma	763	121.5	3.5	1497	2	Q7USA4_RHOBA	Q7uea4 rhodospirillum
691	126.5	3.6	244	2	Q2VCN7_LYCPI	Q2vcn7 lycium pict	764	121.5	3.5	2522	2	Q8EXA6_SHEON	Q8exa6 sheonella
692	126.5	3.6	244	2	Q2VCN8_CUOAL	Q2vcn8 cuon alpinu	765	121	3.5	509	2	Q3FAN3_9BURX	Q3fan3 burholderia
693	126.5	3.6	244	2	Q2VCP1_CANSI	Q2vcp1 canis simen	766	121	3.5	556	2	Q96456_PLAVI	Q96456 plasmodium
694	126.5	3.6	244	2	Q2VCP2_PCARN	Q2vcp2 canis mesom	767	121	3.5	556	2	Q9V1F0_PLAVI	Q9v1f0 plasmodium
695	126.5	3.6	244	2	Q2VCP6_CANAD	Q2vcp6 canis adust	768	121	3.5	1153	1	MAM12_HUMAN	Q81212 homo sapien
696	126.5	3.6	328	2	Q2PF15_MACFA	Q2pf15 macaca fasc	769	121	3.5	1159	2	Q7U7U9_SYNPX	Q7u7u9 synechococc
697	126.5	3.6	454	2	Q9XT09_CAEEL	Q9xt09 caenorhabdi	770	121	3.5	1232	2	Q68219_ANAPH	Q68219 anaplaama p
698	126.5	3.6	659	2	Q4SH26_TETNG	Q4sh26 tetraodon n	771	121	3.5	1232	2	Q9UR07_ANAPH	Q9ur07 anaplaama p
699	126.5	3.6	683	2	Q2KAB7_RHIER	Q2kab7 rhizobium e	772	121	3.5	1598	2	Q60RK8_CABER	Q60rk8 caenorhabdi
700	126.5	3.6	775	1	DCBD2_HUMAN	Q56p2 homo sapien	773	120.5	3.4	630	2	Q2W329_MASSA	Q2w329 magnetospir
701	126	3.6	588	2	Q53QF6_HUMAN	Q53qf6 homo sapien	774	120.5	3.4	929	2	Q642U1_MOUSE	Q642u1 mus musculu
702	126	3.6	664	2	Q91NG4_ARATH	Q91ng4 arabidopsis	775	120.5	3.4	964	1	MK11_MOUSE	Q84316 mus musculu
703	126	3.6	800	2	Q4Y340_PLACH	Q4y340 plasmodium	776	120.5	3.4	964	1	Q3U1I6_MOUSE	Q3u1i6 mus musculu
704	126	3.6	805	2	Q66KFO_XENLA	Q66kfo xenopus lae	777	120.5	3.4	1135	2	Q6BXC0_DEBHA	Q6bxc0 debaryella
705	126	3.6	1649	2	Q57UM9_9TRYP	Q57um9 trypanosoma	778	120.5	3.4	1435	2	Q4ANZ3_THIEPA	Q4anz3 theileria p
706	126	3.6	1649	2	Q8MBR3_9TRYP	Q8mb3 trypanosoma	779	120.5	3.4	2013	2	Q8YPT8_LISMO	Q8ypt8 theileria p
707	126	3.6	3529	2	Q4N9U4_THIEPA	Q4n9u4 theileria p	780	120	3.4	158	2	Q4XHB8_PLACH	Q4xhb8 plasmodium
708	126	3.6	3529	2	Q9GP30_THIEPA	Q9gp30 theileria p	781	120	3.4	510	2	Q94727_PLAVI	Q94727 plasmodium
709	125.5	3.6	244	2	Q2VCM4_VULCH	Q2vcma vulpes cham	782	120	3.4	573	2	MUC13_MOUSE	P19467 mus musculu
710	125.5	3.6	661	2	Q21394_CAEEL	Q21394 caenorhabdi	783	120	3.4	573	2	Q3V1S6_MOUSE	Q3v1s6 mus musculu
711	125.5	3.6	1044	2	Q4AB30_DROME	Q4ab30 dtrosophila	784	120	3.4	747	2	Q7UML2_RHOBA	Q7uml2 rhodospirillum
712	125.5	3.6	1283	1	RF1P1_HUMAN	Q6wkr24 homo sapien	785	120	3.4	922	2	Q6M1H5_BDBEA	Q6m1h5 bdellovibri
713	125.5	3.6	1788	2	Q9VE13_DROME	Q9ve13 dtrosophila	786	120	3.4	939	2	Q8YGR3_ANNAP	Q8ygr3 anabaena bp
714	125	3.6	478	2	Q33082_MYCLE	Q33082 mycobacteri	787	119.5	3.4	123	2	Q41I29_TETNG	Q41i29 tetraodon n
715	125	3.6	586	2	Q9CDD8_MYCLE	Q9cdd8 mycobacteri	788	119.5	3.4	369	2	Q7VTP2_BORPE	Q7vtp2 borrelia
716	125	3.6	769	1	DCBD2_RAT	Q91z2 rattus norv	789	119.5	3.4	468	2	Q55279_ADEGX	Q55279 avian adeno
717	125	3.6	1272	2	Q2UAF6_ASPOR	Q2uaf6 aspergillus	790	119.5	3.4	728	2	Q4OEF23_LEIMA	Q4of23 leishmania
718	125	3.6	1426	2	Q9X3P6_9FIRM	Q9x3p6 caldicellulu	791	119.5	3.4	838	2	Q3M1I6_ANNAT	Q3m1i6 anabaena va
719	125	3.6	2207	2	Q42619_DESHA	Q42619 desulfitoba	792	119.5	3.4	1151	2	Q6CMS9_KLUDIA	Q6cms9 kluyveromyc
720	124.5	3.6	244	2	Q2VCW7_UROCI	Q2vcw7 urocyon cin	793	119.5	3.4	1216	2	Q551S2_CRYNE	Q551s2 cryptococcu
721	124.5	3.6	602	2	Q9Y092_DROME	Q9y092 dtrosophila	794	119.5	3.4	1456	2	Q8Y967_PVX	Q8y967 potlato viru
722	124.5	3.6	925	1	NPAC2_HUMAN	Q6k9r1 oryza sativ	795	119.5	3.4	22152	2	Q8WKT7_HUMAN	Q8wkt7 homo sapien
723	124.5	3.6	1001	2	Q6K9R1_ORYSA	Q6k9r1 oryza sativ	796	119.5	3.4	293	2	Q9S572_DROME	Q9s572 dtrosophila
724	124.5	3.6	1608	2	Q8T5Z6_PLABE	Q8t5z6 plasmodium	797	119	3.4	547	2	Q41700_GIBZE	Q41700 gibberella
725	124.5	3.6	1634	2	Q4YMS7_PLABE	Q4yms7 plasmodium	798	119	3.4	725	1	AGAL_YEAST	P32223 saccharomyc
726	124	3.5	225	2	Q5EBB8_RAT	Q5ebb8 rattus norv	799	119	3.4	1328	1	Q7DU60_ECO57	Q90404 deschaypge o
727	124	3.5	572	2	Q9RC13_LACDL	Q9rc13 lactobacill	800	119	3.4	1588	2	Q7J173_BOVIN	Q7j173 escherichia
728	124	3.5	617	2	Q43NM2_SOLUS	Q43nm2 solibacter	801	119	3.4	143	2	Q7J173_BOVIN	Q7j173 bos taurus
729	124	3.5	769	1	DCBD2_MOUSE	Q91z2 mus musculu	802	118.5	3.4	2013	2	Q4E0Y1_LISMO	P79296 sus scrofa
730	124	3.5	892	2	Q41P94_METBU	Q41p94 methanococc	803	118.5	3.4	227	2	Q8G9M0_RHOBA	Q8g9m0 rhodococcus
731	123.5	3.5	244	2	Q2VCN6_NYCPK	Q2vcn6 nycteraleus	804	118.5	3.4	571	2	Q8G9M0_RHOBA	Q8g9m0 rhodococcus
732	123.5	3.5	697	2	Q4DZP3_TRYCR	Q4dzp3 trypanosoma	805	118.5	3.4	582	2	Q82P59_STRAW	Q82p59 streptomyces
733	123.5	3.5	1456	2	Q9JEX8_PVX	Q9jex8 potlato viru	806	118.5	3.4	627	2	Q6UMH8_TRELE	Q6umh8 treponema l
734	123.5	3.5	1628	2	Q4UAG5_THIEAN	Q4uag5 theileria a	807	118.5	3.4	785	1	CADH7_CHICK	Q90r63 gallus gall
735	123	3.5	421	2	Q41MR7_GIBZE	Q41mr7 gibberella	808	118.5	3.4	1409	2	Q5ALTS_CANAL	Q5alts candida alb
736	123	3.5	506	2	Q4SIC8_TETNG	Q4sic8 tetraodon n	809	118.5	3.4	1699	2	Q911R1_9VIRU	Q911r1 crinean-con
737	123	3.5	740	2	Q4TAR6_TETNG	Q4tar6 tetraodon n	810	118.5	3.4	2013	2	Q4E0Y1_LISMO	Q4egy1 listeria mo
738	123	3.5	1143	2	Q40ZU6_9FIRM	Q40zue eubacterium	811	118.5	3.4	4104	2	Q36E39_9GAMM	Q36e39 shevanelia
739	123	3.5	1203	2	Q9N5K0_CAEEL	Q9n5k0 caenorhabdi	812	118	3.4	508	2	Q39DH7_BURS3	Q39dh7 burholderia
740	123	3.5	2375	2	Q581L4_9CAUD	Q581l4 cyanophaga	813	118	3.4	555	2	Q7XXL2_ORYSA	Q7xxl2 oryza sativ
741	123	3.5	8682	2	Q88RG2_PSEPK	Q88rg2 pseudomonas	814	118	3.4	583	2	Q7XXL2_ORYSA	Q7xxl2 oryza sativ
742	122.5	3.5	244	2	Q2VCP5_CANAU	Q2vcp5 canis aureu	815	118	3.4	609	2	Q8FMW3_CORRE	Q8fmw3 corneobacte
743	122.5	3.5	552	2	Q3SX17_HUMAN	Q3sxy7 homo sapien	816	118	3.4	812	2	Q6CUU0_YARLI	Q6cuu0 yarrowia j
744	122.5	3.5	633	2	Q4CQF5_TRYCR	Q4cqf5 trypanosoma	817	118	3.4	1050	2	Q5EWX9_XENLA	Q5ewx9 xenopus lae
745	122.5	3.5	657	2	Q4MUU0_ASPFU	Q4muu0 aspergillus	818	118	3.4	2733	2	Q9J3E8_9CORO	Q9j3e8 murine hepa
746	122.5	3.5	932	2	Q6K4C3_ORYSA	Q6k4c3 oryza sativ	819	117.5	3.4	915	2	Q8WMM2_HUMAN	Q8wmm2 homo sapien
747	122.5	3.5	1458	2	Q757N5_ASHGO	Q757n5 ashbya gos	820	117.5	3.4	917	1	SMOO_HUMAN	P53814 homo sapien
748	122.5	3.5	1472	2	Q4YAV8_PLABE	Q4yav8 plasmodium	821	117.5	3.4	940	2	Q8WMM1_HUMAN	Q8wmm1 homo sapien
749	122.5	3.5	1744	2	Q82YV8_ENTFA	Q82yv8 enterococcu	822	117.5	3.4	1312	2	Q9YU13_LEIMA	Q9yu13 leishmania
750	122.5	3.5	1814	1	TSC2_MOUSE	Q61037 mus musculu	823	117.5	3.4	1424	2	Q5K868_CRYNE	Q5k868 cryptococcu
751	122.5	3.5	1844	2	Q22579_CAEEL	Q22579 caenorhabdi	824	117.5	3.4	1456	2	Q40DL3_PVX	Q40dl3 potlato viru
752	122	3.5	545	2	Q44019_GAPIC	Q44019 plasmodium	825	117.5	3.4	1808	2	Q3UHB2_MOUSE	Q3ubh2 mus musculu
753	122	3.5	565	2	Q5CKZ9_CRYHO	Q5ckz9 cryptospori	826	117	3.3	552	2	Q3BBQ7_RAT	Q3bbq7 rattus norv
754	122	3.5	1046	2	Q4SMK2_TETNG	Q4sed0 tetraodon n	827	117	3.3	654	2	Q4P1I8_USIMA	Q4p1i8 uncultured
755	122	3.5	1495	2	Q5SMK2_CRYNE	Q5smk2 cryptococcu	828	117	3.3	795	2	Q5MKT4_9ARCH	Q5mkt4 anabaena va
756	122	3.5	1595	2	Q52373_9TRIM	Q52373 caldicellulu	829	117	3.3	939	2	Q3WCU4_ANNAT	Q3wcu4 anabaena va
757	121.5	3.5	244	2	Q2VCP3_CANTU	Q2vcp3 canis lupus	830	117	3.3	1205	2	Q56A66_XENLA	Q56a66 xenopus lae
758	121.5	3.5	244	2	Q2VCP4_CANTU	Q2vcp4 canis latra	831	117	3.3	1213	2	Q7SEF9_NEUCR	Q7sef9 neuropeptora
759	121.5	3.5	253	2	Q8WM25_RHIIA	Q8wm25 rhinopoma h	832	117	3.3	1836	2	Q9LXK4_ARATH	Q9lxx4 arabidopsis
760	121.5	3.5	253	2	Q9UBH1_GAPIC	Q9ubh1 plasmodium	833	117	3.3	2254	2	Q4NED2_THIEPA	Q4ned2 theileria p
761	121.5	3.5	858	2	Q7R0E5_PLAYO	Q7red0 plasmodium	834	117	3.3	2221	2	Q4SED0_TETNG	Q4sed0 tetraodon n

835	117	3.3	2503	2	099136_PRRSV	099136 porcine rep	908	114	3.3	1088	2	05R161_BRARE	05R161 brachydanio
836	116.5	3.3	575	2	08PXL1_XANAC	08PXL1 xanthomonas	909	114	3.3	1431	1	CSK11_HUMAN	CSK11 homo sapien
837	116.5	3.3	756	2	09AEM3_CLODI	09AEM3 clostridium	910	114	3.3	1625	1	06WV4_NEUCR	06WV4 neurospora
838	116.5	3.3	938	1	SEY1_YARLI	06C3b0 yarrowia n	911	114	3.3	1752	2	07R1Y7_GIALA	07R1Y7 giala
839	116.5	3.3	989	2	05NOZ1_ZYMO	05NOZ1 zymomonas m	912	114	3.3	2308	2	083NU3_TROWA	083NU3 tropaeryma
840	116.5	3.3	3300	2	QAN127_THERA	QAN127 theileria p	913	114	3.3	2732	2	04U64_THEAN	04U64 thean
841	116.5	3.3	4567	2	036C93_9GAMM	036C93 shewanella	914	114	3.3	5017	2	081SNO_BACAN	081SNO bacan
842	116	3.3	299	2	03EBD0_ARATH	03EBD0 arabidopsis	915	113.5	3.2	480	2	091SK7_ARATH	091SK7 arabidopsi
843	116	3.3	487	1	ANTR2_MOUSE	06CFX2 mus musculu	916	113.5	3.2	557	2	04R7B7_MACFA	04R7B7 macfa
844	116	3.3	487	2	03CTL6_MOUSE	03CTL6 m mod-deriv	917	113.5	3.2	565	2	05BAU2_EMENT	05BAU2 ementi
845	116	3.3	558	2	06MZG6_HUMAN	06MZG6 homo sapien	918	113.5	3.2	660	2	05LAW1_VIRU	05LAW1 viru
846	116	3.3	629	2	02TY93_ASPOR	02TY93 aspergillus	919	113.5	3.2	716	2	054BH1_DICDI	054BH1 dicdi
847	116	3.3	629	2	04SUQ4_TETNG	04SUQ4 tetradodon n	920	113.5	3.2	725	2	03CRS7_ALTAT	03CRS7 altat
848	116	3.3	775	1	TAU_HYLA	05YCV9 hylobates 1	921	113.5	3.2	815	2	08N536_HUMAN	08N536 human
849	116	3.3	776	2	05CZ17_HUMAN	05CZ17 homo sapien	922	113.5	3.2	951	2	09GLY4_RABIT	09GLY4 rabbit
850	116	3.3	1043	1	GRIP2_FAT	09MTW1 rattus norv	923	113.5	3.2	1123	2	05TOZ1_ANOGA	05TOZ1 anoga
851	116	3.3	1053	2	02RP2_ORYSA	02RP2 oryza sativ	924	113.5	3.2	1153	2	080TK3_MOUSE	080TK3 mouse
852	116	3.3	1161	2	Q7RVQ2_NEUCR	Q7RVQ2 neurospora	925	113.5	3.2	1599	2	04UDB8_THEAN	04UDB8 thean
853	116	3.3	1292	2	06C889_YARLI	06C889 yarrowia 11	926	113.5	3.2	1660	2	03NKN0_LEIMA	03NKN0 leisma
854	116	3.3	1562	2	Q3MP25_CANAL	Q3MP25 candida alb	927	113.5	3.2	1673	2	039BE9_BURS3	039BE9 burs3
855	116	3.3	7176	1	RIAB_CVMA5	PI3342 m replicase	928	113.5	3.2	1982	2	086UD5_DICDI	086UD5 dicdi
856	116	3.3	7178	1	066W16_9COCO	066W16 murine hepa	929	113.5	3.2	2026	2	05S1R4_DICDI	05S1R4 dicdi
857	115.5	3.3	428	1	EEL1_HUMAN	PI9419 homo sapien	930	113.5	3.2	2186	2	054ZN9_DICDI	054ZN9 dicdi
858	115.5	3.3	428	2	06FGS6_HUMAN	06FGS6 homo sapien	931	113.5	3.2	2528	2	086JU6_DICDI	086JU6 dicdi
859	115.5	3.3	454	2	066SR6_HUMAN	066SR6 homo sapien	932	113.5	3.2	507	2	059GR2_HUMAN	059GR2 human
860	115.5	3.3	549	2	06AEJ9_LEIXX	06AEJ9 leifsonia x	933	113	3.2	565	2	04CGT6_CLOTM	04CGT6 clotm
861	115.5	3.3	614	2	Q3FBA2_9BURK	Q3FBA2 burkholderi	934	113	3.2	771	2	0227R3_CAEBL	0227R3 caebel
862	115.5	3.3	688	2	Q4YVA2_PLABE	Q4YVA2 plasmodi	935	113	3.2	775	1	TAU_GORGO	TAU GORGO
863	115.5	3.3	1016	2	Q4HW12_GIBZE	Q4HW12 gibberella	936	113	3.2	775	1	TAU_PANTR	TAU PANTR
864	115.5	3.3	1430	1	CSK11_FAT	08VHK2 rattus norv	937	113	3.2	839	1	055C56_DICDI	055C56 dicdi
865	115.5	3.3	2186	2	08NM19_STEAM	08NM19 streptococ	938	113	3.2	882	2	03GBZ4_PFRM	03GBZ4 pfrm
866	115.5	3.3	2800	2	Q6XHB1_DICDI	Q6XHB1 dictyosteli	939	113	3.2	912	2	05B9Z6_EMENT	05B9Z6 ementi
867	115	3.3	559	1	THD1_LYCES	P25306 lycopersico	940	113	3.2	980	2	07XET5_ORYSA	07XET5 oryza
868	115	3.3	659	2	Q3JNZ6_BURP1	Q3JNZ6 burkholderi	941	113	3.2	1405	2	054GM9_DICDI	054GM9 dicdi
869	115	3.3	843	2	Q35CD8_9BRAD	Q35CD8 bradyrhizob	942	113	3.2	1984	2	Q4MOU1_ASPRU	Q4MOU1 aspru
870	115	3.3	1091	2	Q3BFS8_EMENT	Q3BFS8 aspergillus	943	113	3.2	3956	2	Q9DLN9_PRRSV	Q9DLN9 prrsv
871	115	3.3	1096	2	Q3PH67_PARDE	Q3PH67 paracoccus	944	112.5	3.2	289	2	Q2RZG3_9SPRI	Q2RZG3 9spri
872	115	3.3	1227	2	Q4HYB2_GIBZE	Q4HYB2 gibberella	945	112.5	3.2	386	2	Q40BS4_9RHOB	Q40BS4 9rhob
873	115	3.3	1262	2	Q2ZAJ2_9GAMM	Q2ZAJ2 shewanella	946	112.5	3.2	614	2	08VNU4_LACDL	08VNU4 lacdl
874	115	3.3	1895	2	Q3ORL3_9RHOB	Q3ORL3 silicibacte	947	112.5	3.2	638	1	SRPR_CANPA	SRPR CANPA
875	115	3.3	3966	1	RPOA_PRRS1	Q9YND2 p replicase	948	112.5	3.2	815	2	08N5C4_HUMAN	08N5C4 human
876	114.5	3.3	408	2	Q29129_TDRBR	Q29129 tadarida br	949	112.5	3.2	858	2	055N21_CRYNE	055N21 cryne
877	114.5	3.3	586	2	Q5GQU7_9CAUD	Q5GQU7 bacterioph	950	112.5	3.2	909	2	05XK9F_CRYNE	05XK9F cryne
878	114.5	3.3	620	2	Q7NMY1_CHRYO	Q7NMY1 chromobacte	951	112.5	3.2	858	2	06MP91_BDEBA	06MP91 bdeba
879	114.5	3.3	806	1	SRPR_MOUSE	Q9DBG7 mus musculu	952	112.5	3.2	1015	2	Q2VAT0_CAEBL	Q2VAT0 caebel
880	114.5	3.3	865	2	Q21PF2_9DELT	Q21PF2 anaeromyxob	953	112.5	3.2	1028	2	Q76836_CAEBL	Q76836 caebel
881	114.5	3.3	829	2	Q4N9H1_THERA	Q4N9H1 theileria p	954	112.5	3.2	1075	1	TARSH_HUMAN	TARSH HUMAN
882	114.5	3.3	915	2	Q5R8H9_PONPY	Q5R8H9 pongo pygma	955	112.5	3.2	1087	2	Q7Y4U0_9CAUD	Q7Y4U0 9caud
883	114.5	3.3	931	2	Q91995_XENLA	Q91995 xenopus lae	956	112.5	3.2	1204	2	Q3HHE8_TRIER	Q3HHE8 trier
884	114.5	3.3	1052	2	Q3GCK5_9FIRM	Q3GCK5 syntrophomo	957	112.5	3.2	1309	2	06CC11_YARLI	06CC11 yarli
885	114.5	3.3	1105	2	Q389F7_9TRYP	Q389F7 trypanosoma	958	112.5	3.2	1909	2	Q9LXK3_ARATH	Q9LXK3 arath
886	114.5	3.3	1378	2	Q5L6J2_CHLAB	Q5L6J2 chlamydomo	959	112.5	3.2	1984	2	Q9OBH5_9RHAB	Q9OBH5 rhab
887	114.5	3.3	1542	2	Q5BCK3_EMENT	Q5BCK3 aspergillus	960	112.5	3.2	2186	2	Q5HPI8_STAAC	Q5HPI8 staac
888	114.5	3.3	1756	2	Q7S1S9_ORYSA	Q7S1S9 oryza sativ	961	112	3.2	152	2	Q8WVP6_9ASCI	Q8WVP6 9asci
889	114.5	3.3	16311	2	Q3AR72_CHLCH	Q3AR72 chlorobium	962	112	3.2	231	2	Q8N882_HUMAN	Q8N882 human
890	114	3.3	200	2	Q9Y4S8_HUMAN	Q9Y4S8 homo sapien	963	112	3.2	389	2	Q5ASR4_EMENT	Q5ASR4 ementi
891	114	3.3	227	2	Q6FHW5_HUMAN	Q6FHW5 homo sapien	964	112	3.2	400	2	Q3W769_9ACRO	Q3W769 9acro
892	114	3.3	227	2	Q7LCA7_HUMAN	Q7LCA7 homo sapien	965	112	3.2	484	2	Q91OW1_PSEAE	Q91OW1 pseae
893	114	3.3	237	2	Q3MMW9_9DELT	Q3MMW9 syntrophoba	966	112	3.2	533	2	Q30UL3_THIDN	Q30UL3 thidn
894	114	3.3	563	2	Q9UTU6_TYGB1	Q9UTU6 tygosaacchar	967	112	3.2	555	2	Q9C9Y9_ARATH	Q9C9Y9 arath
895	114	3.3	580	2	Q5VQ66_ORYSA	Q5VQ66 oryza sativ	968	112	3.2	567	2	Q9C9Y9_ARATH	Q9C9Y9 arath
896	114	3.3	597	1	NF2L2_MOUSE	Q6O795 mus musculu	969	112	3.2	575	2	Q74B80_GEOSL	Q74B80 geosl
897	114	3.3	597	1	Q3UOKO_MOUSE	Q3UOKO mus musculu	970	112	3.2	618	2	Q4RH76_TETNG	Q4RH76 tetng
898	114	3.3	628	2	Q4S3J7_TETNG	Q4S3J7 tetradodon n	971	112	3.2	674	2	Q6PMR3_VIRU	Q6PMR3 viru
899	114	3.3	687	2	Q3E273_CHLAD	Q3E273 chloroflexu	972	112	3.2	710	2	Q32914_MYCLE	Q32914 mycle
900	114	3.3	702	2	Q2U444_ASPOR	Q2U444 aspergillus	973	112	3.2	733	2	Q9CB88_MYCLE	Q9CB88 mycle
901	114	3.3	786	2	Q9RZL4_DEIRA	Q9RZL4 deinococcus	974	112	3.2	756	2	Q44YX0_9BURK	Q44YX0 9burk
902	114	3.3	794	2	Q18742_BOVIN	Q18742 bos taurus	975	112	3.2	761	2	Q6MG74_RAT	Q6MG74 rat
903	114	3.3	805	2	Q2QX81_ORYSA	Q2QX81 oryza sativ	976	112	3.2	881	2	Q8GMF9_STRGL	Q8GMF9 strgl
904	114	3.3	820	2	Q18743_BOVIN	Q18743 bos taurus	977	112	3.2	884	2	Q2QIUI9_ORYSA	Q2QIUI9 oryza
905	114	3.3	905	2	Q18741_BOVIN	Q18741 bos taurus	978	112	3.2	925	2	Q2ZGP9_STRSU	Q2ZGP9 strsu
906	114	3.3	1053	2	Q2QNP3_ORYSA	Q2QNP3 oryza sativ	979	112	3.2	1034	2	Q61J69_CAEBR	Q61J69 caebel
907	114	3.3	1053	2	Q94143_ORYSA	Q94143 oryza sativ	980	112	3.2	1053	2	Q7XL61_ORYSA	Q7XL61 oryza sativ

981	112	3.2	1174	2	Q7QC8_ANOCA	Q7qce8 anopheles g	1054	110.5	3.2	1456	1	RDRP_PVX	P0935 potato viru
982	112	3.2	1530	2	Q4P4C4_USTMA	Q4p4c4 ustilago ma	1055	110.5	3.2	1491	2	Q2KAF9_RHIET	Q2kaf9 rhizobium e
983	112	3.2	1557	2	Q06652_DROME	Q06652 drosophila	1056	110.5	3.2	2186	2	Q6GB1_STYAS	Q6gb1 staphylococ
984	112	3.2	1617	2	Q8IK60_PLAF7	Q8ik60 plasmodium	1057	110.5	3.2	2747	2	Q9L800_AERSA	Q9l800 aeromonas s
985	112	3.2	1660	2	Q9SIR1_ARATH	Q9sir1 arabidopsis	1058	110.5	3.2	2771	2	Q4UGJ7_THESN	Q4ugj7 thelleria a
986	112	3.2	1660	2	Q4QERO_LEIMA	Q4qero leishmania	1059	110	3.1	352	1	D0F18_ARATH	Q84j8 arabidopsis
987	112	3.2	2214	2	Q20219_CAEEL	Q20219 caenorhabdi	1060	110	3.1	457	2	Q4RPO3_TETNG	Q4rp3 arabidopsis
988	112	3.2	2503	2	Q4TWM1_PRRSV	Q4twn1 porcine rep	1061	110	3.1	485	2	Q5NXX3_AZOSE	Q5nxx3 azoarcus sp
989	112	3.2	2620	2	Q3NJK2_SHEPR	Q3njk2 shewanella	1062	110	3.1	513	2	Q47B10_DECAR	Q47b10 dechloromon
990	112	3.2	3399	2	Q6LRT5_PHOPE	Q6lrt5 photobacter	1063	110	3.1	562	2	Q67085_GINPA	Q67085 influenza a
991	112	3.2	3960	2	Q9DLN8_PRRSV	Q9dlm8 porcine rep	1064	110	3.1	672	2	Q91VZ8_VIURU	Q91vz8 hepatitis e
992	112	3.2	3960	2	Q9DLP0_PRRSV	Q9dlp0 porcine rep	1065	110	3.1	741	2	Q9P3U2_SCHPO	Q9p3u2 schizosach
993	112	3.2	3960	2	Q9DLP1_PRRSV	Q9dlp1 porcine rep	1066	110	3.1	786	2	Q4UC89_THESN	Q4uc89 thelleria a
994	112	3.2	4333	2	Q36YD8_RHOPE	Q36yd8 rhodopseudo	1067	110	3.1	792	2	Q2RUM5_RHOBU	Q2rum5 rhodospirill
995	111.5	3.2	382	2	Q03990_DAUCA	Q03990 daucus caro	1068	110	3.1	821	2	Q4K9E7_PSEPS	Q4k9e7 pseudomonas
996	111.5	3.2	552	2	Q4N6B9_THEPA	Q4n6b9 thelleria p	1069	110	3.1	827	2	Q5FR97_GLUOX	Q5fr97 gluconobact
997	111.5	3.2	569	2	Q5EF57_9BURK	Q5ef57 acidovorax	1070	110	3.1	846	2	Q4PAA5_USTMA	Q4paa5 ustilago ma
998	111.5	3.2	691	2	Q7NFA4_MYCCA	Q7naf4 mycoplasma	1071	110	3.1	853	2	Q7S3C5_NEUCR	Q7s3c5 neuropept
999	111.5	3.2	699	2	Q3CIY4_PALPH	Q3ciy4 chimpanzee	1072	110	3.1	853	2	Q8YUZE_ANNAP	Q8yuz6 anabaena sp
1000	111.5	3.2	798	2	Q9U225_CAEEL	Q9u225 caenorhabdi	1073	110	3.1	901	2	Q5JUD5_ORYSA	Q5jud5 oryza sativ
1001	111.5	3.2	825	2	Q873Y0_ASPPU	Q873y0 aspergillus	1074	110	3.1	908	2	Q59PF9_CANAL	Q59pf9 candida alb
1002	111.5	3.2	894	2	Q5IFW4_ENTHI	Q5ifw4 entamoeba h	1075	110	3.1	916	2	Q55Y53_CRYNE	Q55y53 cryptococcu
1003	111.5	3.2	989	2	Q94909_HUMAN	Q94909 homo sapien	1076	110	3.1	932	2	Q5LIQ7_ORYSA	Q5liq7 oryza sativ
1004	111.5	3.2	1133	2	Q7SCS8_HUMUR	Q7scs8 neuropept	1077	110	3.1	935	2	Q5AXT3_EMENI	Q5axt3 aspergillus
1005	111.5	3.2	1202	2	Q8MY43_EPTST	Q8my43 eptatretus	1078	110	3.1	940	2	Q2LZ00_DROPS	Q2lzo0 drosophila
1006	111.5	3.2	1320	2	Q4PEJ9_USTMA	Q4pej9 ustilago ma	1079	110	3.1	1006	2	Q55R68_CRYNE	Q55r68 cryptococcu
1007	111.5	3.2	1408	2	Q2UGJ4_ASFOR	Q2ugj4 aspergillus	1080	110	3.1	1006	2	Q5KR02_CRYNE	Q5kr02 cryptococcu
1008	111.5	3.2	1456	2	Q4H4H8_PVX	Q4h4h8 potaro viru	1081	110	3.1	1009	2	Q55R69_CRYNE	Q55r69 cryptococcu
1009	111.5	3.2	1678	2	Q3UGI8_MOUSE	Q3ugi8 mus musculu	1082	110	3.1	1009	2	Q55R69_CRYNE	Q55r69 cryptococcu
1010	111.5	3.2	1742	2	Q7TJ21_MOUSE	Q7tj21 mus musculu	1083	110	3.1	1027	2	Q37LP3_RHOPE	Q37lp3 rhodopseudo
1011	111.5	3.2	1984	2	Q9QBH1_PRRAB	Q9qbh1 viral hemor	1084	110	3.1	1057	2	Q4PSX6_USTMA	Q4psx6 ustilago ma
1012	111.5	3.2	1984	2	Q9QVJ4_PRRAB	Q9qvj4 viral hemor	1085	110	3.1	1073	2	Q6C0R9_YARLT	Q6cor9 yarrowia ll
1013	111.5	3.2	1984	2	Q9QVJ0_PRRAB	Q9qvj0 viral hemor	1086	110	3.1	1094	2	Q7RX91_NEUCR	Q7rx91 neuropept
1014	111.5	3.2	8173	2	Q7UDU8_RHOBA	Q7udu8 rhodopirell	1087	110	3.1	1110	2	Q55P47_CRYNE	Q55p47 cryptococcu
1015	111	3.2	327	2	Q2MM20_STRTR	Q2mm20 streptococc	1088	110	3.1	1110	2	Q55KEA9_CRYNE	Q55kea9 cryptococcu
1016	111	3.2	332	2	Q4KCM1_PSEPS	Q4kcm1 pseudomonas	1089	110	3.1	1148	2	Q7TS92_MOUSE	Q7ts92 mus musculu
1017	111	3.2	342	2	Q54VJ1_DICDI	Q54vj1 dictyosteli	1090	110	3.1	1155	2	Q3UHF2_MOUSE	Q3uhf2 mus musculu
1018	111	3.2	381	2	Q6Z5E1_CAEER	Q6z5e1 caenorhabdi	1091	110	3.1	1160	2	Q924U7_MOUSE	Q924u7 mus musculu
1019	111	3.2	445	2	Q89F39_BRJUA	Q89f39 bradyrhizob	1092	110	3.1	1205	2	Q9LAT9_ANNAP	Q9lat9 annaelsma p
1020	111	3.2	531	2	Q365I3_9GAMA	Q365i3 shewanella	1093	110	3.1	1205	2	Q9RPM8_ANNAP	Q9rpm8 anagallia p
1021	111	3.2	562	2	Q67I20_9INFA	Q67i20 influenza a	1094	110	3.1	1351	2	Q31V22_SHIBS	Q31v22 shigella bo
1022	111	3.2	582	2	Q7NSP1_CHRVO	Q7nsf1 chromobact	1095	110	3.1	1367	1	MUC1_YEAST	Q61c8 saccharomyc
1023	111	3.2	598	2	Q31EN8_THICK	Q3ien8 thiomicrosp	1096	110	3.1	1367	2	Q61CS8_SACDI	Q61c8 saccharomyc
1024	111	3.2	757	2	Q31IK5_THICK	Q3iik5 thiomicrosp	1097	110	3.1	1456	2	Q91KX2_PVX	Q91kx2 potato viru
1025	111	3.2	850	2	Q3N2X5_9DELTA	Q3n2x5 syntrophoba	1098	110	3.1	1731	2	Q4Q981_LEIMA	Q4q981 leishmania
1026	111	3.2	860	2	Q4RR4_TETNG	Q4rr4 tetraodon n	1099	110	3.1	1986	2	Q4WU47_ASPPU	Q4wu47 aspergillus
1027	111	3.2	924	2	Q5KLT6_CRYNE	Q5klt6 cryptococcu	1100	109.5	3.1	384	2	Q8GVG6_ORYSA	Q8gv6 oryza sativ
1028	111	3.2	1002	2	Q8GZY5_ORYSA	Q8gzy5 oryza sativ	1101	109.5	3.1	387	2	Q4AD265_TRYCR	Q4ad265 trypanosoma
1029	111	3.2	1004	2	Q8PU63_METMA	Q8pu63 methanocarc	1102	109.5	3.1	560	2	Q91965_MYCSY	Q91965 mycoplasma
1030	111	3.2	1053	2	Q2R4K7_ORYSA	Q2r4k7 oryza sativ	1103	109.5	3.1	622	2	Q7SR50_NEUCR	Q7sr50 neuropept
1031	111	3.2	1085	2	Q3DW7_STRAG	Q3dw7 streptococc	1104	109.5	3.1	633	2	Q4WN71_ASPPU	Q4wn71 aspergillus
1032	111	3.2	1115	2	Q3S2Y8_STRAG	Q3s2y8 streptococc	1105	109.5	3.1	638	2	Q5RAC7_PONPY	Q5rac7 pongo pygma
1033	111	3.2	1189	2	Q5CTA0_CRYPV	Q5cta0 cryptospori	1106	109.5	3.1	648	2	Q41B25_GIBZE	Q41b25 gibberella
1034	111	3.2	1194	2	Q6BYH4_DEBNA	Q6byh4 debaryomyce	1107	109.5	3.1	667	1	K0431_HUMAN	Q43h3 homo sapien
1035	111	3.2	1205	2	Q49RA6_STRAG	Q49ra6 streptococc	1108	109.5	3.1	779	2	Q4H084_PREDI	Q4h084 fireyella d
1036	111	3.2	1222	2	Q8MY44_EPTST	Q8my44 eptatretus	1109	109.5	3.1	862	2	Q3PRR4_NITHA	Q3pr4 nitroabacter
1037	111	3.2	1239	2	Q7X5P9_ANNAP	Q7x5p9 annaplasma p	1110	109.5	3.1	987	2	Q4Y3Z3_PLACH	Q4y3z3 plasmodium
1038	111	3.2	1241	2	Q8LL04_ARATH	Q8ll04 arabidopsis	1111	109.5	3.1	1077	2	Q448G5_SOLUS	Q448g5 solibacter
1039	111	3.2	1578	2	Q57YR3_XTRYP	Q57yr3 trypanosoma	1112	109.5	3.1	1151	2	Q55L95_CRYNE	Q55l95 cryptococcu
1040	111	3.2	2037	2	Q9PVZ2_ENTELA	Q9pvz2 xenopus lae	1113	109.5	3.1	1151	2	Q5XAB9_CRYNE	Q5xab9 cryptococcu
1041	111	3.2	2503	2	Q9ENK6_PRRSV	Q9enk6 porcine rep	1114	109.5	3.1	1469	2	Q3KW17_GRHIZ	Q3kw17 mesorhizobi
1042	111	3.2	3960	1	RPOA_PRRSV	Q9wj2 p replicase	1115	109.5	3.1	1809	1	TSC2_RAT	Q9816 ratius nov
1043	110.5	3.2	409	2	Q8IR01_DROME	Q8ir01 drosophila	1116	109.5	3.1	1984	2	Q9WME7_PRRAB	Q9wme7 viral hemor
1044	110.5	3.2	504	2	Q6J4Y8_CHICK	Q6j4y8 gallus galli	1117	109.5	3.1	3181	2	Q6MKN7_PARRU	Q6mkn7 parichlamyd
1045	110.5	3.2	695	2	Q2U6F7_ASPPU	Q2u6f7 aspergillus	1118	109.5	3.1	4408	2	Q44AC0_SOLUS	Q44ac0 solibacter
1046	110.5	3.2	779	2	Q50588_PSEHY	Q50588 pseudomonas	1119	109.5	3.1	4920	2	Q4KXF3_PSEPS	Q4kxf3 pseudomonas
1047	110.5	3.2	815	2	Q8MWL6_HUMAN	Q8mw6 homo sapien	1120	109.5	3.1	7342	2	Q3XG91_9PROT	Q3xg91 magnetococ
1048	110.5	3.2	885	2	Q5XK5_CRYNE	Q5xk5 cryptococcu	1121	109	3.1	720	2	Q9A3H3_CAUCR	Q9a3h3 caubacter
1049	110.5	3.2	885	2	Q5KAQ0_CRYNE	Q5kaq0 cryptococcu	1122	109	3.1	302	2	Q43UAD2_SOLUS	Q43uad2 solibacter
1050	110.5	3.2	1040	1	IF2_BACYN	Q8a2a1 bacteroides	1123	109	3.1	452	2	Q9SC06_ARATH	Q9sc06 arabidopsis
1051	110.5	3.2	1066	1	Q22804_ARATH	Q22804 arabidopsis	1124	109	3.1	489	1	ANTR2_HUMAN	P58333 homo sapien
1052	110.5	3.2	1081	1	MED15_YEAST	P19659 s rna polym	1125	109	3.1	496	2	Q6ZTGI_HUMAN	Q6ztgi homo sapien
1053	110.5	3.2	1176	2	Q3AZB7_SYNS9	Q3azb7 synechococ	1126	109	3.1	795	2	Q96PV6_HUMAN	Q96pv6 homo sapien

1127	109	3.1	802	2	Q19764_CAEEL	Q19764 caenorhabdi	1200	108	3.1	538	2	Q6SPF0_HUMAN	Q6SPF0 homo sapien
1128	109	3.1	806	2	Q9VH91_DROME	Q9VH91 drosophila	1201	108	3.1	562	2	Q4ZH98_9INPA	Q4ZH98 influenza a
1129	109	3.1	851	2	Q4H023_CAMPUR	Q4H023 campylobact	1202	108	3.1	562	2	Q67123_9INPA	Q67123 influenza a
1130	109	3.1	927	2	Q93G12_MORBO	Q93G12 moraxella b	1203	108	3.1	572	2	Q2Y910_NITMU	Q2Y910 nitrospir
1131	109	3.1	985	2	Q94J41_ORYSA	Q94J41 oryza sativ	1204	108	3.1	581	2	Q4QC23_LEIMA	Q4QC23 leishmania
1132	109	3.1	987	2	Q65WY6_ORYSA	Q65WY6 oryza sativ	1205	108	3.1	623	2	Q41MF3_METHU	Q41MF3 methanococ
1133	109	3.1	1053	2	Q60F03_ORYSA	Q60F03 oryza sativ	1206	108	3.1	635	2	Q612N5_CAEAR	Q612N5 caenorhabdi
1134	109	3.1	1053	2	Q5VP31_ORYSA	Q5VP31 oryza sativ	1207	108	3.1	645	2	Q9H048_HUMAN	Q9H048 homo sapien
1135	109	3.1	1091	2	Q06556_STRDY	Q06556 streptococc	1208	108	3.1	660	2	Q9YLK2_VIRU	Q9YLK2 hepatitis e
1136	109	3.1	1102	2	Q872D9_NEUCR	Q872D9 neurospora	1209	108	3.1	674	2	Q6BD83_VIRU	Q6BD83 hepatitis e
1137	109	3.1	1159	2	Q3PRW7_NITHA	Q3PRW7 nitrobacter	1210	108	3.1	674	2	Q7TG11_VIRU	Q7TG11 hepatitis e
1138	109	3.1	1182	2	Q24552_DROME	Q24552 drosophila	1211	108	3.1	674	2	Q8UJN2_VIRU	Q8UJN2 hepatitis e
1139	109	3.1	1182	2	Q9VC05_DROME	Q9VC05 drosophila	1212	108	3.1	675	2	Q4WP66_ASPPU	Q4WP66 aspergillus
1140	109	3.1	1187	2	Q8MY42_EPTST	Q8MY42 eptretus	1213	108	3.1	706	2	Q47M06_THERY	Q47M06 thermobifid
1141	109	3.1	1242	2	Q9W005_DROME	Q9W005 drosophila	1214	108	3.1	757	1	TAU_HUMAN	TAU homo sapien
1142	109	3.1	1253	2	Q7XT19_ORYSA	Q7XT19 oryza sativ	1215	108	3.1	759	2	Q2UGV8_ASPPR	Q2UGV8 aspergillus
1143	109	3.1	1425	2	Q86CW3_DROSE	Q86CW3 drosophila	1216	108	3.1	768	2	Q9VH92_DROME	Q9VH92 hepatitis e
1144	109	3.1	1602	2	Q4PCU7_USTMA	Q4PCU7 ustilago ma	1217	108	3.1	777	2	Q311J7_THICK	Q311J7 thiomicrosp
1145	109	3.1	1614	2	Q69Y09_HUMAN	Q69Y09 homo sapien	1218	108	3.1	784	2	Q8INN6_DROME	Q8INN6 drosophila
1146	109	3.1	1739	2	Q4W2V7_PLARE	Q4W2V7 plasmodium	1219	108	3.1	803	2	Q6A065_MOUSE	Q6A065 mus musculu
1147	109	3.1	1756	2	Q6AMK8_DROME	Q6AMK8 drosophila	1220	108	3.1	823	2	Q39ES1_BUR83	Q39ES1 burkholderi
1148	109	3.1	1785	2	Q3UG88_MOUSE	Q3UG88 mus musculu	1221	108	3.1	836	2	Q7XXY2_ARATH	Q7XXY2 arabidopsis
1149	109	3.1	1872	2	Q6FYV5_BAROU	Q6FYV5 bartonella	1222	108	3.1	906	2	Q54WV3_DICDI	Q54WV3 dictyosteli
1150	109	3.1	1928	2	Q4PB06_USTMA	Q4PB06 ustilago ma	1223	108	3.1	931	2	Q7S500_NEUCR	Q7S500 neurospora
1151	109	3.1	5017	2	Q81FJ0_BACCR	Q81FJ0 bacillus ce	1224	108	3.1	998	2	Q12869_HUMAN	Q12869 homo sapien
1152	108.5	3.1	300	2	Q35E19_9BRAD	Q35E19 bradyrhizob	1225	108	3.1	1053	2	Q5VM23_ORYSA	Q5VM23 oryza sativ
1153	108.5	3.1	421	2	Q4YQV5_PLABE	Q4YQV5 plasmodium	1226	108	3.1	1156	2	Q2KX10_RHIEF	Q2KX10 rhizobium e
1154	108.5	3.1	490	2	Q58315_9TRYP	Q58315 trypanosoma	1227	108	3.1	1231	2	Q85170_ANAPH	Q85170 anaplasmia p
1155	108.5	3.1	490	2	Q968P6_PLAVI	Q968P6 plasmodium	1228	108	3.1	1231	2	Q7BS35_ANAPH	Q7BS35 anaplasmia p
1156	108.5	3.1	606	2	P90573_PLABE	P90573 plasmodium	1229	108	3.1	1231	2	Q9JRL4_9RICK	Q9JRL4 ehrlichia s
1157	108.5	3.1	629	2	Q4USY6_XANCP	Q4USY6 xanthomonas	1230	108	3.1	1231	2	Q9JUR03_ANAPH	Q9JUR03 anaplasmia p
1158	108.5	3.1	639	2	Q8PAN0_XANCP	Q8PAN0 xanthomonas	1231	108	3.1	1242	2	Q6N306_RHOPA	Q6N306 rhodospo
1159	108.5	3.1	639	2	Q3MHB8_BOVIN	Q3MHB8 bos taurus	1232	108	3.1	1262	2	Q35XK2_9GAMV	Q35XK2 shewanella
1160	108.5	3.1	652	1	U1P2_SCHPO	U1P2 schistosomach	1233	108	3.1	1268	1	SC24B_HUMAN	SC24B homo sapien
1161	108.5	3.1	660	2	Q514T2_9VIRU	Q514T2 hepatitis e	1234	108	3.1	1289	2	Q6P4R6_HUMAN	Q6P4R6 homo sapien
1162	108.5	3.1	660	2	Q514T5_9VIRU	Q514T5 hepatitis e	1235	108	3.1	1344	2	Q15312_HUMAN	Q15312 homo sapien
1163	108.5	3.1	678	2	Q2QR67_ORYSA	Q2QR67 oryza sativ	1236	108	3.1	1520	2	Q4PB06_USTMA	Q4PB06 ustilago ma
1164	108.5	3.1	681	2	Q9FFW5_ARATH	Q9FFW5 arabidopsis	1237	108	3.1	1556	2	Q91BE1_FUGRU	Q91BE1 fugu rubrip
1165	108.5	3.1	682	2	Q3TY26_MOUSE	Q3TY26 mus musculu	1238	108	3.1	1634	2	Q9XW25_CAEEL	Q9XW25 caenorhabdi
1166	108.5	3.1	682	2	Q3ULB5_MOUSE	Q3ULB5 mus musculu	1239	108	3.1	1640	2	Q3F3K8_9BURK	Q3F3K8 burkholderi
1167	108.5	3.1	724	2	Q9H6S7_HUMAN	Q9H6S7 homo sapien	1240	108	3.1	1698	2	Q55WE2_CRYNE	Q55WE2 cryptococcu
1168	108.5	3.1	738	2	Q5B3B1_EMENT	Q5B3B1 aspergillus	1241	108	3.1	1870	2	Q7SDE6_NEUCR	Q7SDE6 neurospora
1169	108.5	3.1	784	2	Q58ER8_BRARE	Q58ER8 brachydanio	1242	108	3.1	1977	2	Q83TF5_STRCZ	Q83TF5 streptomyce
1170	108.5	3.1	860	2	Q6J614_ENTCL	Q6J614 enterobacte	1243	108	3.1	2728	2	Q583U1_9TRYP	Q583U1 trypanosoma
1171	108.5	3.1	866	2	Q5KEA7_CRYNE	Q5KEA7 cryptococcu	1244	108	3.1	4007	2	Q7SHZ4_NEUCR	Q7SHZ4 neurospora
1172	108.5	3.1	877	2	Q6DMK4_ENTCL	Q6DMK4 enterobacte	1245	108	3.1	10495	2	Q4R892_TETNG	Q4R892 tetradospo
1173	108.5	3.1	881	2	Q2KI05_BORAV	Q2KI05 bordetella	1246	107.5	3.1	172	2	Q5GN53_MYOCO	Q5GN53 mycoaspor c
1174	108.5	3.1	954	2	Q3FCR7_DBURK	Q3FCR7 burkholderi	1247	107.5	3.1	201	2	Q4XHC4_PLACH	Q4XHC4 plasmidoma
1175	108.5	3.1	971	2	Q6W3C4_CAEEL	Q6W3C4 caenorhabdi	1248	107.5	3.1	263	2	Q8MUV6_SCHHA	Q8MUV6 schistosoma
1176	108.5	3.1	989	2	Q19930_CAEEL	Q19930 caenorhabdi	1249	107.5	3.1	355	2	Q7W152_BORPA	Q7W152 borrelia
1177	108.5	3.1	995	2	Q69V30_ORYSA	Q69V30 oryza sativ	1250	107.5	3.1	363	2	Q31JH9_THICK	Q31JH9 thiomicrosp
1178	108.5	3.1	1188	2	Q7PPI1_ANOGA	Q7PPI1 anopheles g	1251	107.5	3.1	386	2	Q4CZ98_TRYCR	Q4CZ98 trypnosoma
1179	108.5	3.1	1209	1	TR16_MOUSE	TR16 mus musculu	1252	107.5	3.1	509	2	Q8ZC12_YERPE	Q8ZC12 yerstinia pe
1180	108.5	3.1	1376	2	Q7SHH8_NEUCR	Q7SHH8 neurospora	1253	107.5	3.1	513	2	Q3X577_9PROT	Q3X577 magnetococc
1181	108.5	3.1	1409	1	RPOC_RALSO	RPOC talistonia s	1254	107.5	3.1	539	2	Q3W8S0_9ACTO	Q3W8S0 frantilia sp.
1182	108.5	3.1	1513	2	Q5XNH8_CRYNE	Q5XNH8 cryptococcu	1255	107.5	3.1	636	2	Q3KRC3_RAT	Q3KRC3 rattus norv
1183	108.5	3.1	1623	2	Q4R6X3_TETNG	Q4R6X3 tetradospo	1256	107.5	3.1	644	1	SF04_RAT	SF04 rattus norv
1184	108.5	3.1	1689	2	Q8QZFA_9VIRU	Q8QZFA cricmean-con	1257	107.5	3.1	667	2	Q6BNC9_HUMAN	Q6BNC9 homo sapien
1185	108.5	3.1	1689	2	Q991H9_9VIRU	Q991H9 cricmean-con	1258	107.5	3.1	674	2	Q5B9S6_EMENT	Q5B9S6 aspergillus
1186	108.5	3.1	1779	2	Q52374_PFTIM	Q52374 caldicellu	1259	107.5	3.1	792	2	Q6FYB5_CANGA	Q6FYB5 candida gla
1187	108.5	3.1	1826	2	Q7QK99_ANOGA	Q7QK99 anopheles g	1260	107.5	3.1	810	2	Q7UUV8_RHOBA	Q7UUV8 rhodopirell
1188	108.5	3.1	1845	2	Q3NZ54_9GAMM	Q3NZ54 shewanella	1261	107.5	3.1	833	2	Q5B418_EMENT	Q5B418 aspergillus
1189	108.5	3.1	2732	2	Q9J3F2_9CORO	Q9J3F2 murine hepa	1262	107.5	3.1	940	2	Q7XTN8_ORYSA	Q7XTN8 oryza sativ
1190	108.5	3.1	2733	2	Q7NN3_9CORO	Q7NN3 murine hepa	1263	107.5	3.1	954	2	Q59PV2_CANAL	Q59PV2 candida alb
1191	108.5	3.1	3269	2	Q9RGN5_LACRE	Q9RGN5 lactobacill	1264	107.5	3.1	964	2	Q38DK5_9TRYP	Q38DK5 trypanosoma
1192	108.5	3.1	7124	1	RIAB_CW2	RIAB replicase	1265	107.5	3.1	977	2	Q6KJ19_ORYSA	Q6KJ19 oryza sativ
1193	108	3.1	242	2	Q3PH3_NITHA	Q3PH3 nitrobacter	1266	107.5	3.1	1051	2	Q43WV4_SOLUS	Q43WV4 solibacter
1194	108	3.1	316	2	Q6CV2_YARLI	Q6CV2 yarrowia li	1267	107.5	3.1	1170	1	SCAR4_ARATH	SCAR4 arabidopsis
1195	108	3.1	417	2	Q84NK6_ORYSA	Q84NK6 oryza sativ	1268	107.5	3.1	1208	2	Q4PEL0_USTMA	Q4PEL0 ustilago ma
1196	108	3.1	480	2	Q66T11_XENLA	Q66T11 xenopus lae	1269	107.5	3.1	1249	2	Q59X47_CANAL	Q59X47 candida alb
1197	108	3.1	511	1	EGRI_BRARE	EGRI brachydanio	1270	107.5	3.1	1256	2	Q6PD75_ERWCT	Q6PD75 erwina car
1198	108	3.1	512	2	Q4ZYG5_PSEU2	Q4ZYG5 pseudomonas	1271	107.5	3.1	1260	2	Q2UBW2_ASPPR	Q2UBW2 aspergillus
1199	108	3.1	537	2	Q41NS5_GIBZE	Q41NS5 gibberella	1272	107.5	3.1	1501	2	Q9SD86_ARATH	Q9SD86 arabidopsis

1273	107.5	3.1	1604	2	055JP5_CRYNE	055JP5_cryptococcu	1346	106.5	3.0	794	1	PMS1_SCHPO	P54280_schizosacch
1274	107.5	3.1	1689	2	08QZP5_VIRU	08qz5 crimean-con	1347	106.5	3.0	800	1	KIN4_YEAST	Q01919 saccharomyc
1275	107.5	3.1	1747	2	05PAP1_ANAMU	05pap1 anaplasmu	1348	106.5	3.0	841	2	0847M6_HELPY	0847m6 hellicobacte
1276	107.5	3.1	1899	2	0303R2_STRSU	0303r2 streptococc	1349	106.5	3.0	931	2	0916S5_BACPI	0916s5 bacillus f1
1277	107.5	3.1	2112	2	09VEI9_DROME	09vei9 diptrophilla	1350	106.5	3.0	966	2	07PKN8_ANOGA	07pkn8 anopheles g
1278	107.5	3.1	2642	2	02ZRO9_SHEPU	02zr9 shewanella	1351	106.5	3.0	1047	2	074BT1_GEOSL	074bt1 geobacter s
1279	107.5	3.1	2644	2	02X787_9GAMM	02x787 shewanella	1352	106.5	3.0	1058	2	0851R2_ORYSA	0851r2 oryza sativ
1280	107	3.1	363	1	LYPD3_MOUSE	091ykr mus musculu	1353	106.5	3.0	1161	2	09EP53_MOUSE	09ep53 mus musculu
1281	107	3.1	371	2	03RU03_RALME	03ru03 ralsobium s	1354	106.5	3.0	1269	2	03P5Z6_NITRA	03p5z6 nitrobacter
1282	107	3.1	404	2	06W222_RHISM	06w222 rhizobium s	1355	106.5	3.0	1322	2	08MSX3_DROME	08msx3 dirosophila
1283	107	3.1	432	2	05G197_BACCT	05g197 bacillus ci	1356	106.5	3.0	1343	2	06CX33_YARLI	06cx33 yarrowia l1
1284	107	3.1	513	2	08G5K3_EIFLU	08g5k3 bifidobacte	1357	106.5	3.0	1382	2	05KRK2_CRYNE	05krk2 cryptococcu
1285	107	3.1	550	2	06SPE9_RABIT	06spe9 oryctolagus	1358	106.5	3.0	1431	2	03ME76_ANAVT	03me76 anabaena va
1286	107	3.1	562	2	067333_IASIN	067333 influenza a	1359	106.5	3.0	1501	2	02UBK5_ASPPR	02ubk5 aspergillus
1287	107	3.1	612	2	08CID1_MOUSE	08cid1 mus musculu	1360	106.5	3.0	1543	2	07K5S6_DROME	07k5s6 dirosophila
1288	107	3.1	616	2	06KZZ0_PICTO	06kzz0 picophilus	1361	106.5	3.0	1578	2	09BMW9_HUMAN	09bmw9 homo sapien
1289	107	3.1	616	2	099K31_MOUSE	099k31 mus musculu	1362	106.5	3.0	1658	2	03LHL9_DROME	03lhl9 dirosophila
1290	107	3.1	674	2	06BD78_VIRU	06bd78 hepaticis e	1363	106.5	3.0	1728	2	03PWE1_NITRA	03pwe1 nitrobacter
1291	107	3.1	683	2	04SBR2_TETNG	04sbr2 tetradon n	1364	106.5	3.0	1761	2	07LBC6_HUMAN	07lbc6 homo sapien
1292	107	3.1	704	2	04MM72_ASPPU	04mm72 aspergillus	1365	106.5	3.0	1787	2	09UP50_HUMAN	09up50 homo sapien
1293	107	3.1	774	2	05SLQ1_CRYNE	05slq1 cryptococcu	1366	106.5	3.0	2139	2	04PDM0_USTWA	04pdm0 ustilago ma
1294	107	3.1	774	2	05K9Z2_CRYNE	05k9z2 cryptococcu	1367	106.5	3.0	2272	2	06NR00_DROME	06nr00 dirosophila
1295	107	3.1	774	2	05KDB7_CRYNE	05kdb7 cryptococcu	1368	106.5	3.0	2727	2	09VU06_DROME	09vu06 dirosophila
1296	107	3.1	789	2	06CS14_KLUUA	06cs14 kluyveromyc	1369	106.5	3.0	5094	2	021ZL4_RHOPA	021z14 rhodopseudo
1297	107	3.1	835	2	07UY68_RHOB	07uy68 rhodopiteil	1370	106	3.0	351	2	039492_CHLEU	039492 chlamydomon
1298	107	3.1	856	2	09SY11_ARATH	09sy11 arabidopsis	1371	106	3.0	456	2	02VYMO_MAGSA	02vy00 magnetospir
1299	107	3.1	880	2	084WV4_ARATH	084wv4 arabidopsis	1372	106	3.0	480	2	04UQJ2_9GAMM	04uqj2 methyllobac
1300	107	3.1	880	2	094C84_ARATH	094c84 arabidopsis	1373	106	3.0	523	2	03SBR1_9BRAD	03sbr1 brachyribzob
1301	107	3.1	930	2	040X22_KINRA	040x22 kinococcus	1374	106	3.0	531	2	022367_9GAMM	022367 shewanella
1302	107	3.1	944	2	07RY29_NEUCR	07ry29 neurospora	1375	106	3.0	550	2	08UYV3_VIRU	08uyv3 hepatitis e
1303	107	3.1	964	2	05GX30_XANOR	05gx30 xanthomonas	1376	106	3.0	602	2	05SKL2_DROME	05skl2 dirosophila
1304	107	3.1	1053	2	05VMS2_ORYSA	05vms2 oryza sativ	1377	106	3.0	604	2	05KDO3_CRYNE	05kdo3 cryptococcu
1305	107	3.1	1070	2	02PI06_ASPPR	02pi06 aspergillus	1378	106	3.0	613	2	060F93_ORYSA	060f93 oryza sativ
1306	107	3.1	1163	1	TSCI1_RAT	09zi16 rattus norv	1379	106	3.0	633	2	046UJ3_PROMT	046uj3 prochloroco
1307	107	3.1	1196	2	05H935_HUMAN	05h935 homo sapien	1380	106	3.0	636	2	08JTN4_LSDPY	08jtn4 lumby skin
1308	107	3.1	1200	2	05TPW6_ANOGA	05tpw6 anopheles g	1381	106	3.0	671	2	08JUM1_VIRU	08jum1 hepatitis e
1309	107	3.1	1205	2	02W610_MAGSA	02w610 magnetospir	1382	106	3.0	674	2	08JUN6_VIRU	08jun6 hepatitis e
1310	107	3.1	1231	2	06CL75_KLUUA	06cl75 kluyveromyc	1383	106	3.0	680	2	0217P4_VIRU	0217p4 bacterioph
1311	107	3.1	1245	2	03A968_CARHZ	03a968 carboxyloth	1384	106	3.0	691	2	09RZS7_DEIRA	09rzs7 diennococcus
1312	107	3.1	1264	2	07PD01_PLAYO	07pd01 plasmodium	1385	106	3.0	752	2	02UB42_ASPPR	02ub42 aspergillus
1313	107	3.1	1266	2	09VG10_DROME	09vg10 dirosophila	1386	106	3.0	785	2	054CE0_DICDI	054ce0 dicystostell
1314	107	3.1	1308	2	09DF77_CHICK	09df77 gallus gall	1387	106	3.0	830	2	059FN4_HUMAN	059fn4 homo sapien
1315	107	3.1	1350	2	02P7F6_XANOR	02p7f6 xanthomonas	1388	106	3.0	838	2	05AV13_EMENT	05av13 aspergillus
1316	107	3.1	1350	2	05H4M5_XANOR	05h4m5 xanthomonas	1389	106	3.0	839	1	IF2_HAEPU	07v112 haemophilus
1317	107	3.1	1412	2	05SIX9_CRYNE	05s1x9 cryptococcu	1390	106	3.0	857	2	06IRG8_RAT	06irg8 rattus norv
1318	107	3.1	1412	2	05KCS4_CRYNE	05kcs4 cryptococcu	1391	106	3.0	949	2	06ODP1_RAT	06odp1 rattus norv
1319	107	3.1	1450	2	09CE07_LACIA	09ce07 lactococcus	1392	106	3.0	963	2	09P759_NEUCR	09p759 neurospora
1320	107	3.1	1616	2	03YVW7_SHISS	03yv7 shigella so	1393	106	3.0	966	2	07KX78_ORYSA	07kx78 oryza sativ
1321	107	3.1	2887	2	03KGA0_PSEBP	03kga0 pseudomonas	1394	106	3.0	974	2	04K0Z7_ASPPU	04k0z7 aspergillus
1322	107	3.1	2911	2	03JES9_BURPI	03jes9 burkholderi	1395	106	3.0	996	2	08B3W1_PSSSM	08b3w1 pseudomonas
1323	107	3.1	2931	2	03EVR2_BACPI	03evr2 bacillus th	1396	106	3.0	1050	2	04PD88_USTWA	04pd88 ustilago ma
1324	107	3.1	4540	2	07P5S5_ANOGA	07p5s5 anopheles g	1397	106	3.0	1060	2	07RYW5_NEUCR	07ryw5 neurospora
1325	107	3.1	5017	2	063DP3_BACCZ	063df3 bacillus ce	1398	106	3.0	1072	1	MAP4_BOVIN	P36225 bos taurus
1326	106.5	3.0	206	2	05SP07_BRARE	05sp07 brachydanio	1399	106	3.0	1085	2	06BD12_HUMAN	06bd12 homo sapien
1327	106.5	3.0	355	2	07MN02_BORER	07mn02 bordetella	1400	106	3.0	1123	2	08E106_DICDI	08e106 d bamlilar t
1328	106.5	3.0	358	2	04K040_PSEFS	04k40 pseudomonas	1401	106	3.0	1130	1	LATS1_HUMAN	095335 homo sapien
1329	106.5	3.0	363	2	03WB68_9ACTO	03wb68 frankia sp.	1402	106	3.0	1148	2	06MPH0_BDBBA	06mph0 bdellovibri
1330	106.5	3.0	363	2	03WH13_9ACTO	03wh13 frankia sp.	1403	106	3.0	1151	2	07S4R8_NEUCR	07s4r8 neurospora
1331	106.5	3.0	380	2	02LE02_9ACTO	02le02 streptomyces	1404	106	3.0	1235	2	06TEN8_BRARE	06ten8 brachydanio
1332	106.5	3.0	465	2	091M88_ARATH	091m88 arabidopsis	1405	106	3.0	1269	2	05V2A6_HALMA	05v2a6 halocaula
1333	106.5	3.0	490	2	03RT16_PALME	03rt16 ralsobium m	1406	106	3.0	1281	2	09V795_DROME	09v795 dirosophila
1334	106.5	3.0	503	2	07NUJ9_GLOVI	07nuj9 gloeobacter	1407	106	3.0	1335	2	04PIR5_USTWA	04pir5 ustilago ma
1335	106.5	3.0	574	2	03V3A8_MOUSE	03v3a8 mus musculu	1408	106	3.0	1375	2	05SR47_CRYNE	05sr47 cryptococcu
1336	106.5	3.0	606	2	03GYU2_9ACTO	03gyu2 nocardioide	1409	106	3.0	1415	2	09HCF4_HUMAN	09hcf4 homo sapien
1337	106.5	3.0	638	1	SRPR_HUMAN	P08320 homo sapien	1410	106	3.0	1473	2	06ICV7_XANGC	06icv7 xanthomonas
1338	106.5	3.0	660	2	02Z1X2_VIRU	02z1x2 hepatitis e	1411	106	3.0	1523	2	0813B1_PLA7	0813b1 plasmodium
1339	106.5	3.0	673	2	02UD04_ASPPR	02ud04 aspergillus	1412	106	3.0	1534	2	09UID9_HUMAN	09uid9 homo sapien
1340	106.5	3.0	694	2	0541Q2_DICDI	0541q2 dicystostell	1413	106	3.0	1597	2	05IDB1_ENTHI	05ide1 entomoba h
1341	106.5	3.0	703	2	06LVY7_XANOR	06lv7 phorbacter	1414	106	3.0	1699	2	05KJY6_CRYNE	05kji6 cryptococcu
1342	106.5	3.0	713	2	08PU00_XANAC	08pu00 xanthomonas	1415	106	3.0	1729	2	05SPB1_CRYNE	05spb1 cryptococcu
1343	106.5	3.0	721	1	YCHD_SGHP	09y7v2 schizosacch	1416	106	3.0	1770	2	09X3P5_9PIRM	09x3p5 caldicellul
1344	106.5	3.0	756	2	06RT13_PHOPR	06rt13 photobacter	1417	106	3.0	2027	2	08UW52_FUGRM	08uw52 fugu rubrip
1345	106.5	3.0	792	2	05FR09_GLUOX	05fr09 gluconobacter	1418	106	3.0	2111	2	04SOH1_TETNG	04soh1 tetradon n

1419	106	3.0	2497	2	Q7YZ94_DROME
1420	106	3.0	2497	2	Q96806_DROME
1421	106	3.0	2797	2	Q81V72_HUMAN
1422	106	3.0	3183	2	Q8MLW2_DROME
1423	106	3.0	3198	2	Q917V8_DROME
1424	106	3.0	3201	2	Q9NDJ2_DROME
1425	106	3.0	4135	2	Q34EW3_DROME
1426	105.5	3.0	363	2	Q3VXF0_9ACTO
1427	105.5	3.0	363	2	Q3W7T6_9ACTO
1428	105.5	3.0	378	2	Q19568_CAEEL
1429	105.5	3.0	410	2	Q56AV3_9ACTO
1430	105.5	3.0	421	2	Q15329_HUMAN
1431	105.5	3.0	480	2	Q8SXK1_DROME
1432	105.5	3.0	480	2	Q3JCA9_NITOC
1433	105.5	3.0	513	2	Q9NHP8_DROME
1434	105.5	3.0	528	2	Q9ZPL6_TOBAC
1435	105.5	3.0	572	2	Q390V1_GEOMG
1436	105.5	3.0	606	2	Q2U6D9_ASFOR
1437	105.5	3.0	638	2	Q6TAX9_HUMAN
1438	105.5	3.0	650	2	Q55J47_CRYNE
1439	105.5	3.0	684	2	Q7XHM7_ORYSA
1440	105.5	3.0	688	2	Q916G6_LACDE
1441	105.5	3.0	721	2	Q591J1_CANAL
1442	105.5	3.0	738	2	Q4PBG2_USTMA
1443	105.5	3.0	753	2	Q2Y2P2_GINCI
1444	105.5	3.0	814	2	Q55AJ1_DICDI
1445	105.5	3.0	817	1	VRA1_YEAST
1446	105.5	3.0	817	2	Q07229_YEAST
1447	105.5	3.0	818	2	Q418U1_GIBZE
1448	105.5	3.0	827	1	SSP2_PLAYO
1449	105.5	3.0	878	2	Q3U241_MOUSE
1450	105.5	3.0	887	2	Q239J3_DICDI
1451	105.5	3.0	915	2	Q4QRH6_BRARE
1452	105.5	3.0	974	2	Q3SIG5_RALME
1453	105.5	3.0	1015	2	Q4UMG2_XANCF
1454	105.5	3.0	1015	2	Q8P7N8_XANCF
1455	105.5	3.0	1043	2	Q97E41_CLOAB
1456	105.5	3.0	1082	2	Q4RUC4_TETNG
1457	105.5	3.0	1108	2	Q2K7J1_MAGGR
1458	105.5	3.0	1140	2	Q40BN7_9RHOB
1459	105.5	3.0	1206	2	Q9JRC4_ANAPH
1460	105.5	3.0	1223	2	Q9JRC6_ANAPH
1461	105.5	3.0	1232	2	Q8MXD2_DROME
1462	105.5	3.0	1240	2	Q9JRM5_ANAPH
1463	105.5	3.0	1253	2	Q9W111_DROME
1464	105.5	3.0	1299	2	Q9NSM8_HUMAN
1465	105.5	3.0	1371	2	Q3TWM2_MOUSE
1466	105.5	3.0	1371	2	Q8BV57_MOUSE
1467	105.5	3.0	1415	2	Q3YN49_BACTK
1468	105.5	3.0	1521	2	Q8CHS9_MOUSE
1469	105.5	3.0	1524	2	Q4POB8_USTMA
1470	105.5	3.0	1744	2	Q6PAR1_HUMAN
1471	105.5	3.0	1748	1	POIR_ELV
1472	105.5	3.0	1748	2	Q549I0_ELV
1473	105.5	3.0	1789	2	Q838B3_9CALI
1474	105.5	3.0	1918	2	Q54F48_DICDI
1475	105.5	3.0	2112	2	Q80U93_MOUSE
1476	105.5	3.0	2133	2	Q7WRQ2_STANU
1477	105.5	3.0	2364	2	Q4UEI6_THEAN
1478	105.5	3.0	2590	2	Q7ONQ7_GITALA
1479	105	3.0	367	2	Q8U961_AGRIS
1480	105	3.0	412	2	Q7CTH6_AGRIS
1481	105	3.0	420	2	Q2YD66_BOVIN
1482	105	3.0	449	2	Q9H2K4_HUMAN
1483	105	3.0	464	2	Q431U3_SOLUS
1484	105	3.0	501	2	Q44CB9_CHRSL
1485	105	3.0	506	2	Q2RV63_RHORI
1486	105	3.0	516	2	Q54Z21_DICDI
1487	105	3.0	546	2	Q3MGJ3_ANAVT
1488	105	3.0	562	1	HEMA_IATAP
1489	105	3.0	562	2	Q67144_9INFA
1490	105	3.0	566	2	Q55521_CRYNE
1491	105	3.0	566	2	Q5KHG3_CRYNE

Q7YZ94	dtrosophila
Q96806	dtrosophila
Q81V72	homo sapien
Q8MLW2	dtrosophila
Q917V8	dtrosophila
Q9NDJ2	dtrosophila
Q34EW3	rhodopsin
Q3VXF0	frankia sp.
Q3W7T6	frankia sp.
Q19568	caenorhabditis
Q56AV3	gordonia de
Q15329	homo sapien
Q8SXK1	dtrosophila
Q3JCA9	nitrosococc
Q9NHP8	dtrosophila
Q9ZPL6	nicotiana t
Q390V1	geobacter m
Q2U6D9	aspergillus
Q6TAX9	homo sapien
Q55J47	cryptococcu
Q7XHM7	oryza sativ
Q916G6	lactobacill
Q591J1	candida alb
Q4PBG2	usciilago ma
Q2Y2P2	gingilymesto
Q55AJ1	dictyosteli
P37370	saccharomyc
Q07229	saccharomyc
Q418U1	gibberella
Q01443	plasmodium
Q3U241	m nod-deriv
Q239J3	dictyosteli
Q4QRH6	brachydanio
Q3SIG5	relaxona m
Q4UMG2	xanthomonas
Q8P7N8	xanthomonas
Q97E41	clostridium
Q4RUC4	tetrazodon
Q2K7J1	magnaporthe
Q40BN7	jannaschia
Q9JRC4	anaplasmia p
Q9JRC6	anaplasmia p
Q8MXD2	dtrosophila
Q9JRM5	anaplasmia p
Q9W111	dtrosophila
Q9NSM8	homo sapien
Q3TWM2	mus musculu
Q8BV57	mus musculu
Q3YN49	bacillus th
Q8CHS9	mus musculu
Q4POB8	usciilago ma
Q6PAR1	homo sapien
P35928	eyasium la
Q549I0	eyasium la
Q838B3	normalk vir
Q54F48	dictyosteli
Q80U93	mus musculu
Q7WRQ2	staphylococ
Q4UEI6	theileria a
Q7ONQ7	gracilaria lam
Q8U961	agrobacteri
Q7CTH6	agrobacteri
Q2YD66	bos taurus
Q9H2K4	homo sapien
Q431U3	solibacter
Q44CB9	chromohalob
Q2RV63	rhodospirill
Q54Z21	dictyosteli
Q3MGJ3	anabaena va
P37370	influenza a
Q67144	influenza a
Q55521	cryptococcu
Q5KHG3	cryptococcu

1492	105	3.0	585	2	Q8H501_ORYSA
1493	105	3.0	597	1	NP212_RAT
1494	105	3.0	604	2	Q6P7C8_RAT
1495	105	3.0	621	2	Q89ZB2_BACTIN
1496	105	3.0	621	2	Q4SNW3_TETNG
1497	105	3.0	660	2	Q36613_9VIRU
1498	105	3.0	660	2	Q36613_9VIRU
1499	105	3.0	660	2	Q6J8F7_9VIRU
1500	105	3.0	660	2	Q6J8G3_9VIRU
1501	105	3.0	660	2	Q801R7_9VIRU

ALIGNMENTS

RESULT 1

06UX17_HUMAN	PRELIMINARY; PRT; 678 AA.
06UX17_HUMAN	24-MAY-2005, integrated into UniProtKB/TrEMBL.
06UX17_HUMAN	24-MAY-2005, sequence version 1.
06UX17_HUMAN	07-FEB-2006, entry version 4.
06UX17_HUMAN	VIT.
06UX17_HUMAN	ORFNames=UN0647;
06UX17_HUMAN	Homo sapiens (human).
06UX17_HUMAN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
06UX17_HUMAN	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
06UX17_HUMAN	Homo.
06UX17_HUMAN	NCBI_TaxID=9606;
06UX17_HUMAN	11
06UX17_HUMAN	NUCLEOTIDE SEQUENCE.
06UX17_HUMAN	MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
06UX17_HUMAN	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
06UX17_HUMAN	Chen J., Chow B., Chu C., Crowley C., Currell B., Deuel B., Dowd P.,
06UX17_HUMAN	Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
06UX17_HUMAN	Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,
06UX17_HUMAN	Lewis L., Lao D., Mark W.R., Robble E., Sanchez C., Schoenfeld J.,
06UX17_HUMAN	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
06UX17_HUMAN	Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
06UX17_HUMAN	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
06UX17_HUMAN	Wood W.I., Godowski P.J., Gray A.M.;
06UX17_HUMAN	"The secreted protein discovery initiative (SPDI), a large-scale
06UX17_HUMAN	effort to identify novel human secreted and transmembrane proteins: a
06UX17_HUMAN	bioinformatics assessment.";
06UX17_HUMAN	Genome Res. 13:2265-2270(2003).
06UX17_HUMAN	-----
06UX17_HUMAN	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
06UX17_HUMAN	Distributed under the Creative Commons Attribution-NonDerivs License
06UX17_HUMAN	-----
06UX17_HUMAN	EMBL; AY358338; AA08704.1; -; mRNA.
06UX17_HUMAN	HSSP; OA3405; 1JBI.
06UX17_HUMAN	InterPro; IPR004043; LCCL.
06UX17_HUMAN	InterPro; IPR002035; VWF_A.
06UX17_HUMAN	Pfam; PF03815; LCCL; 1.
06UX17_HUMAN	Pfam; PF00092; VMA; 2.
06UX17_HUMAN	PRINTS; PR00453; VWFADOMAIN.
06UX17_HUMAN	SMART; SM00603; LCCL; 1.
06UX17_HUMAN	SMART; SM00327; VMA; 2.
06UX17_HUMAN	PROSITE; PSS00820; LCCL; 1.
06UX17_HUMAN	PROSITE; PSS0234; VWF_A; 2.
06UX17_HUMAN	SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;
06UX17_HUMAN	Query Match 100.0%; Score 3502; DB 2; Length 678;
06UX17_HUMAN	Best Local Similarity 100.0%; Pred. No. 3e-219;
06UX17_HUMAN	Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
06UX17_HUMAN	1 MTRVVLTMASVTEMLVLLVTGSHNKKETAKKIKPKFTVPOINDVAKGKTIIDPEFIV 60
06UX17_HUMAN	1 MTRVVLTMASVTEMLVLLVTGSHNKKETAKKIKPKFTVPOINDVAKGKTIIDPEFIV 60
06UX17_HUMAN	KCPAGQODPKRVHYGYGVDAVSYSVCGAIVHSGVLNDSGKILVRAVAGOSGKYSVNG 120
06UX17_HUMAN	KCPAGQODPKRVHYGYGVDAVSYSVCGAIVHSGVLNDSGKILVRAVAGOSGKYSVNG 120

QY 241 PRADPGIQRDPGSAAGKPVGADVSL-----GLVPKEELSTQSLPEVSL 285
 Db 241 PRADPGIQRDPGSAAGKPVGADVSLGEMDSMKRGSVLDEGLVPKEELSTQSLPEVSL 300
 QY 286 GDRPNCKIDLSLIDGSTS IGRRRRIQKOLLADVAQALDIGPAPLMGVVOYGNDPATHF 345
 Db 301 GDRPNCKIDLSLIDGSTS IGRRRRIQKOLLADVAQALDIGPAPLMGVVOYGNDPATHF 360
 QY 346 NLKHTNSRDLKTAIEKTORGSLSNVGRASIFVTKNFFSKANGNSGAPNVVVVVMDGW 405
 Db 361 NLKHTNSRDLKTAIEKTORGSLSNVGRASIFVTKNFFSKANGNSGAPNVVVVVMDGW 420
 QY 406 PTDKVEASRLARSGINIFITTEGAENKQYVVEBNFANKAVCRITNGFYSLHVSWF 465
 Db 421 PTDKVEASRLARSGINIFITTEGAENKQYVVEBNFANKAVCRITNGFYSLHVSWF 480
 QY 466 GLHKTLOPLVKRVDCTDLRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLKEF 525
 Db 481 GLHKTLOPLVKRVDCTDLRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLKEF 540
 QY 526 EISPTDRIGAVOYTYEORLEFEGFDKYSKXPDILNAIKRVGWSGCTGTGAINFALBOL 585
 Db 541 EISPTDRIGAVOYTYEORLEFEGFDKYSKXPDILNAIKRVGWSGCTGTGAINFALBOL 600
 QY 586 FKSKSPNKRKLMILITDGRSYDVRIIPMAAHLKGVITTYAIGVMAAOEBLEVIATHPAR 645
 Db 601 FKSKSPNKRKLMILITDGRSYDVRIIPMAAHLKGVITTYAIGVMAAOEBLEVIATHPAR 660
 QY 646 DHSFVDEFDNLHOYVRRIITNICTEFNPSOPRN 678
 Db 661 DHSFVDEFDNLHOYVRRIITNICTEFNPSOPRN 693

RESULT 3

Q96DT1_HUMAN PRELIMINARY; PRT; 656 AA.
 ID Q96DT1_HUMAN
 AC Q96DT1
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Vitrin.
 GN Name=VIT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Skeletal muscle;
 RA Ren Z.-X., Liu J.G., Mayne R.,
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 CC EMBL: AF063833; AAL18263.1; -, mRNA.
 DR HSSP: Q43405; 1JBI.
 DR InterPro: IPR004043; LCCL.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF03815; LCCL; 1.
 DR Pfam: PF00092; VMA; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SM00603; LCCL; 1.
 DR SMART: SM00327; VMA; 2.
 DR PROSITE: PS50820; LCCL; 1.
 DR PROSITE: PS50234; VWF_A; 2.
 SQ SEQUENCE 656 AA; 71768 MW; E242E0D0FB07CF2C CRC64;

Query March 95.5% Score 3344; DB 2; Length 656;
 Best Local Similarity 96.0%; Pred. No. 5.7e-209;
 Matches 651; Conservative 1; Mismatches 4; Indels 22; Gaps 1;

QY 1 MRTVLTMKASVIEMLVLLVTGVSNKETAKIKRKFTVPQINCVDKAKGIIIDPEFIV 60
 Db 1 MRTVLTMKASVIEMLVLLVTGVSNKETAKIKRKFTVPQINCVDKAKGIIIDPEFIV 60
 QY 61 KCPAGCDDPKHYHYGTDVYASYSVCGAAVHSGVLNDSGKKILVRKAGSGYKGSYNG 120
 Db 61 KCPAGCDDPKHYHYGTDVYASYSVCGAAVHSGVLNDSGKKILVRKAGSGYKGSYNG 120
 QY 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
 Db 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
 QY 181 PVTLMQLAATVAVAFTTLPSPSPASSTSIIPROSVGRSQEMDLMTATYTSQNR 240
 Db 181 PVTLMQLAATVAVAFTTLPSPSPASSTSIIPROSVGRSQEMDLMTATYTSQNR 240
 QY 241 PRADPGIQRDPGSAAGKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
 Db 241 PRADP-----GLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 278
 QY 301 STSIGRRRIQKOLLADVAQALDIGPAPLMGVVOYGNDPATHFNLKHTNSRDLKTAI 360
 Db 279 STSIGRRRIQKOLLADVAQALDIGPAPLMGVVOYGNDPATHFNLKHTNSRDLKTAI 338
 QY 361 EKTORGSLSNVGRASIFVTKNFFSKANGNSGAPNVVVVVMDGWPTDKVEASRLAR 420
 Db 339 EKTORGSLSNVGRASIFVTKNFFSKANGNSGAPNVVVVVMDGWPTDKVEASRLAR 398
 QY 421 GINIFITTEGAENKQYVVEBNFANKAVCRITNGFYSLHVSFGIHLKTLOPLVKRVD 480
 Db 399 GINIFITTEGAENKQYVVEBNFANKAVCRITNGFYSLHVSFGIHLKTLOPLVKRVD 458
 QY 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLKEFISDPTDRIGAVOYT 540
 Db 459 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLKEFISDPTDRIGAVOYT 518
 QY 541 YEORLFEGFDKYSKXPDILNAIKRVGWSGCTGTGAINFALBOLFKSKSPNKRKLMILI 600
 Db 519 YEORLFEGFDKYSKXPDILNAIKRVGWSGCTGTGAINFALBOLFKSKSPNKRKLMILI 578
 QY 601 TDRGSYDVRIIPMAAHLKGVITTYAIGVMAAOEBLEVIATHPARHDSFVDEFDNLHOY 660
 Db 579 TDRGSYDVRIIPMAAHLKGVITTYAIGVMAAOEBLEVIATHPARHDSFVDEFDNLHOY 638
 QY 661 VPRITNICTEFNPSOPRN 678
 Db 639 VPRITNICTEFNPSOPRN 656

RESULT 4

Q37Z47_MOUSE PRELIMINARY; PRT; 650 AA.
 ID Q37Z47_MOUSE
 AC Q37Z47
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Adult inner ear cDNA, RIKEN full-length enriched library,
 DE clone: F930022K14 product: vitrin, full insert sequence.
 GN Name=VIT;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; Tissue=inner ear;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44 (1999).
 [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frich M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmshaw L.G., Aldonis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhury V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgianni-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gurjivani S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Lunj S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottequati-Taber S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nelson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
RA Schombach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tanno K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hilde W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RC (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the mammalian transcriptome.";
RL Science 309:1564-1566(2005).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishio T., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglert D.R., Melais L., Marchionni L., McKenzie L., Miki H.,
RA Nagasima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Teasdale R.D., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilmshaw L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki N.,
RA Hirokawa-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Myazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nishio T., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bono M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gurjivani S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmshaw L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiyosawa T., Tashiro H., Itoh M.,
RA Sami N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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EMBL: AK158117; BAE34363.1; --; mRNA.
DR MGI: MGI11921449; Vlt.


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Db      510 QYTYEORLQFGDPKYNKADILSIRRVGWSGTGAAIQAVALQELFKSKRNKRKM 569
QY      598 ILITDGSYDDVRIIPAMAHLKGVITTAIGVAMAQOELEVIATHPARHSPFVDEPNL 657
Db      570 IITIDGSYDDVRIIPAMAHLKGVITTAIGVAMAQOELEVIATHPARHSPFVDEPNL 629
QY      658 HQYVPRRIIONICTEFNSOPRN 678
Db      630 YKIAPRRIIONICTEFNSOPRN 650

RESULT 6
Q9SLI2_BOVIN PRELIMINARY; PRT; 652 AA.
ID      Q9SLI2_BOVIN
AC      Q9SLI2;
DT      01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT      01-MAR-2002, sequence version 2.
DT      07-FEB-2006, entry version 16.
DE      Vitilin.
GN      Name=VIT;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Retina;
RA      Ren Z.-X., Liu J.G., Wayne R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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CC      -----
EMBL; AF063832; AALJ8262.2; -; mRNA.
DR      HSSP; OA4305; 1JBI.
DR      InterPro; IPR004043; LCCL.
DR      InterPro; IPR002035; VWF_A.
DR      Pfam; PF03815; LCCL; 1.
DR      Pfam; PF00092; VMA; 2.
DR      PRINTS; PR00453; VWFADOMAIN.
DR      SMART; SM00603; LCCL; 1.
DR      SMART; SM00327; VMA; 2.
DR      PROSITE; PS50820; LCCL; 1.
DR      PROSITE; PS50234; VWF_A; 2.
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Db      181 PVLMLQILAATVAVATPTTLPRPSPASATTSIPRPOVGHRSQEMDLMSATATYSSQNR 240
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QY      227 --GEP-----ALMKPESVLLDAGFVPKEELSTQSLSPASQDGPSCVDLSFLIDG 274
Db      227 --GEP-----ALMKPESVLLDAGFVPKEELSTQSLSPASQDGPSCVDLSFLIDG 274
QY      301 STSGKRFRRIQKOLLADVQAQLDIGAGPLMGVVGNDPAPTHFNKTHTNRSDLKTAI 360
Db      301 STSGKRFRRIQKOLLADVQAQLDIGAGPLMGVVGNDPAPTHFNKTHTNRSDLKTAI 360

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Db      275 SSSIGRRRRIQKOLLADVQAQLDIGAPGLMGVVGNDPAPTHFNKTHTNRSQVKAII 334
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Db      335 EKISQKGLSNVGRASIFVTKNFFSKANGRSAGPANNVVVVWDGWPETDKEASRLARS 394
QY      421 GINIFPITTEGAENKQYVEPNFANKVCRITNGFYSLHVOSFGLKHTLOPLVKRVD 480
Db      395 GVINIFPITTEGAENKQYVEPNFANKVCRITNGFYSLHVOSFGLKHTLOPLVKRVD 454
QY      481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNLTKEEISPTDRIGVOYT 540
Db      455 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVNLTKEEISPTDRIGVOYT 514
QY      541 YEORLEFGFDKYSKKEDINAIKRVGVWSGTSTGAINFALQELFKSKPNKRKLMILI 600
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QY      601 TDRGSYDDVRIIPAMAHLKGVITTAIGVAMAQOELEVIATHPARDHSFFVDEPNLHQY 660
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RESULT 7
Q8K047_MOUSE PRELIMINARY; PRT; 650 AA.
ID      Q8K047_MOUSE
AC      Q8K047;
DT      01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT      01-OCT-2002, sequence version 1.
DT      07-FEB-2006, entry version 18.
DE      Vitilin.
GN      Name=Vit;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Eye;
RA      MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lonnegren N.A., Peters G.J., Abramson R.D., Mallat S.J.,
RA      Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA      Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Eye;
RA      Director MGC Project;
RL      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC034120; AAH34120.1; -; mRNA.
DR HSSP; 043405; IUBI.
DR Ensemble; ENSMUSG0000024076; Mus musculus.
DR MGI; MGI:1921449; Vlt.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VMPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
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Query Match      80.0%; Score 2801; DB 2; Length 650;
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DB 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLNDSGKILVRKVAAGSGYKYSNG 120
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DB 121 VQSLSPRWRESFVLSSKPKGYTPSALTYSSSKSPAAGATTAYORPPIPTTAAQ 180
QY 181 PVTLIMOLAVAVATPTLTPRPSPSAATTSIRPQSVGHRSGDEM--DLMSATATYSS 237
DB 181 PVTLIMOLAVAVATPTLTPRPSPSAATTSIRPQSVGHRSGDEM--DLMSATATYSS 237
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DB 238 QNRPRADPGIQRDPGSAFQKPYGADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFL 297
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DB 418 RESGINIFITIEGAENEEKQYVEPNFANKAVCRINGFYSLHVQSWFGLHKTLOPLVKR 477
QY 478 VCDTRDLACSTKCLNSADIGFVINDGSSVGTGNRTVLQPTNLTKEFEISDTRIGAV 537
DB 478 VCDTRDLACSTKCLNSADIGFVINDGSSVGTGNRTVLQPTNLTKEFEISDTRIGAV 537
QY 538 QYTEQRLERGFQDYKSKPDLINAIKVGWYWSGSGTGAANFALDELFFKSKRNKRKLM 597
DB 538 QYTEQRLERGFQDYKSKPDLINAIKVGWYWSGSGTGAANFALDELFFKSKRNKRKLM 597
QY 598 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAAQOELEVIATHPARDSFFVDEPDL 657
DB 598 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAAQOELEVIATHPARDSFFVDEPDL 657
QY 658 HOYVPRITONICTEFNOPRN 678
DB 658 HOYVPRITONICTEFNOPRN 678
QY 630 YKLAIRITONICTEFNOPRN 650
DB 630 YKLAIRITONICTEFNOPRN 650

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AC O9CYZ1;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE 10, 11 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:2810429K11 product:VITRIN, full insert sequence.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aldison V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
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RA di Bernhardt D., Down T., Engstrom P., Fagioli M., Faulkner G.,
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RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Uchi M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Lium S., McMillan S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
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RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempel C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Telchmann S.A.,
RA Ueda H.R., Van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
RA Yamamoto S., Zabarovsky E., Zhu S., Zimmer A., Zlotnick C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawasashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Teganu M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;

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RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi I., Bono H., Kondo S.,
 RA Nakazaki I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gotohori T.,
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 RA Schirrm L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Dalia E., Dragani T.A., Fletcher V., Chochia C., Corbani L.E., Cousins S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
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 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konegaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,
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 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varadero R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Zhao Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi I., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
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 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schirrm L.M., Schirrm L.F., Suzuki R., Tomita M., Wagner L., Watanabe Y.,
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 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guinchich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 RL
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA "Normalization and subtractions of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
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 RN
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC MEDLINE=20350913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuhiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-Format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
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 RP STRAIN=C57BL/6J; TISSUE=Whole body;
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi I., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
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 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Iizawa M., Kasukawa T., Kato H.,
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 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Yamamura T., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK013193; BAB28702.1; -; mRNA.
 DR HSP: O43405; IJBI.
 DR Ensembl: ENSMUSG00000024076; Mus musculus.
 DR MGI: MGI:1921449; Vlt.
 DR GO: GO:0005615; Cytoplasmic space; RCA.
 DR InterPro: IPR004043; LCCL.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF03815; LCCL; 1.
 DR Pfam: PF03092; VMA; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SM00603; LCCL; 1.
 DR SMART: SM00327; VMA; 2.
 DR PROSITE: PS00820; LCCL; 1.
 DR PROSITE: PS0234; VWF; 2.
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 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE 12 days embryyo spinal ganglion cDNA, RIKEN full-length enriched
 DE library, clone:DI30059M21 product:VIRIN homolog.
 GN Name=Vlt;
 OS Mus musculus (Mouse).
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 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
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 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Method Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=1641072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Bajic V.B., Bremner S.G., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.U., Wilmink L.G., Aldin V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
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 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RL Science 309:1559-1563(2005).
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 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=1641073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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 RA Mikaido I., Oseko N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
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 RA Blake J.A., Brad D., Bruce V., Choehia C., Corbett L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Girmond S., Gustincich S., Hirokawa N., Jackson J.D., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziercki R.M., King B.L.,
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 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
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 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
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 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
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 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21055660; PubMed=11217851; DOI=10.1038/35055500;
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 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
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Db      345 ISLSVSSSREARSAVERKITQKGLSHVGRALSTINQYFSDAANGNAAVNAVVLVDG 404
Qy      405 WPTDKVEASRLARESGINIFITIEGAANEKQVVEPNFANKAVCRTNGFYSIAVQSW 464
Db      405 WPTDKVEASRLARESGINIFITIEGPDLGEKQVVEHDPVDAVCRITSGFELPSSW 464
Qy      465 FGLHKLQPLVKRYCDTRLACSRTCLNSADIGVLDGSSVGTGNRTVLQFVNTLKE 524
Db      465 FARKLVQPLVKRYCDTRLVCSKTCCLNANDIAFVIGSSSVGTGNFRTVLQFVANTIRE 524
Qy      525 FEISDITRIGAVOYTEORLEFGFDKYSSKPDILNAIKRYVSGSTGGAIAINFALQ 584
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Qy      585 LFKSKENKRLMLITDGRSYDVRIPAMAHLKGVITVAI--GVMAAQEELVIATH 642
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RESULT 12

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Q8AN56_BRARE PRELIMINARY; PRT; 553 AA.
AC O8AN56;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Novel protein similar to human coagulation factor C homolog (Cochlin,
DE COCH).
GN Name=Coch; Synonyms=OTTDARP0000001491; ORFNames=d2234G15.4-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Babbage A.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AL596026; CAD58748.1; -, Genomic DNA.
DR HSSP; 043405; 1JBI.
DR Ensembl; ENSDARG000000024032; Danio rerio.
DR ZFIN; ZDB-GENE-030616-403; coch.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
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Db 5 FAVLVLHVLITSLWCSGSELNVATP-----ISCGTRAVDLSDTHLLVCPANCISLWSL 58

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Db      59 SVYSGGVASISSICGAIHRGIIIGLSGGEVVEHNGQRTNIVSSVAHGQVQSGSLQWSA 118
Qy      132 SFTVLESKPKKGVTPSALTYSKSPAAQAGETTYAQRPIPGTTAOPVTLMQLLAVT 191
Db      119 SF-----
Qy      192 VAVATPTTLPRPSAASITSTIPRQSVGHRSGEMDLMSTATYTSSQNPRAADPGIQRD 251
Db      121 -TVARTISLPLEVYSSQTSSTAV----- 142
Qy      252 PSGARQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDSTSIGKRRFR 311
Db      143 ASGAA-KKPVKK-----IYKK-----PPRTAHKDCQVDWALLDSSVNIQGRFNL 188
Qy      312 QKQLADVAAQALDIGAGPLMGVQGDNPATFENLKTHTNSRDLKTAIEKITQROGLSN 371
Db      189 QKNFVKRLATMLKVQGGPHVGVQTSPTPEFYLNTYTTADVFALKEIPIYGNTN 248
Qy      372 VGRALSFVTNPFSSKANGRSGAPNVVWVVDGPTDKVEASRLARESGINIFITIEG 431
Db      249 TGRALHTVNFSPDPFGVRGRGIPRYIVFVDSGMBDNEBAAILARESGINIFVSVAK 308
Qy      432 AAENEKQVVEPNFANKAVCRTNGFYSIAVQSWFGLHKLQPLVKRYCDTRLACSKTCL 491
Db      309 PSPBEASIVSDQPMKAKVCKDNEFTFTMPGSMFSTNKKVPLAQGLCSIDQMLGSKTCV 368
Qy      492 NSADIGFVIDGSSSVGTGNFRTVLQFVNTLKEFEISDITRIGAVOYTEORLEFGFDK 551
Db      369 NSVDLGFLLIDGSSSVGDGNFRLVLLVSIARFSDIGSRGAIQFTYDQMEPNFD 428
Qy      552 YSSKPDILNAIKRYVSGSTGGAIAINFALBEDLFKSKPNKRLMLITDGRSYDVRP 611
Db      429 HVKDNALRLQKITPMSGRTATGDAINPAVNSLFPBRSSNRKFLIITDQSYDVRV 488
Qy      612 PAMAHLKGVITVAIGVMAAAQEELEVIATHPARDSFVDFPNLHQYVPRITONIC-- 669
Db      489 PAMAAGREGITVAVGVMAAPMEDLKAMASEPKESHVFTREPTGLGQOQPIVRGICRD 548
Qy      670 -TEFN 673
Db      549 FTEFN 553

```

RESULT 13

```

ID COCH_CHICK STANDARD; PRT; 547 AA.
AC 042163;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Cochlin precursor (COCH-SB2).
GN Name=COCH; Synonyms=COCHSB2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP STAGE.
RC STRAIN=White leghorn; TISSUE=Basilar papilla;
RX MEDLINE=98409669; Pubmed=9736748; DOI=10.1073/pnas.95.19.11400;
RA Heller S., Sheane C.A., Javed Z., Hudepeth A.J.;
RT "Molecular markers for cell types of the inner ear and candidate genes
RT for hearing disorders.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).
CC -!- SUBCELLULAR LOCATION: Secreted protein (potential).
CC -!- TISSUE SPECIFICITY: Expressed in inner ear structures; the
CC spindle-shaped cells of the basilar papilla. Weaker expression
CC found in the inferior and superior fibrocartilaginous plates and

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CC skeletal muscle.
CC -1- DEVELOPMENTAL STAGE: Specifically expressed at the late
CC developmental stages in the cochlea.
CC -1- SIMILARITY: Contains 1 LCCL domain.
CC -1- SIMILARITY: Contains 2 WMA domains.
CC -1- DATABASE: NAME=Protein Spotlight; NOTE=Issue 4 of November 2000;
CC WWW="http://www.expasy.org/spotlight/back_issues/spl004.shtml".
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
DR EMBL: AF012252; AAC62253.1; -. mRNA.
DR HSSP: O43405; 1UBI.
DR Ensembl: ENSGALG0000009920; Gallus gallus.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR002035; WMA_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; WMA; 2.
DR PRINTS: PR00453; WMADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; WMA; 2.
DR PROSITE: PS00820; LCCL; 1.
DR PROSITE: PS00234; WMA; 2.
DR GlycoProtein: Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 19 Potential.
FT CHAIN 20 547 Cochlin.
FT FTID=PRO_0000020967.
FT DOMAIN 24 117 LCCL.
FT DOMAIN 162 347 WMA 1.
FT DOMAIN 364 534 WMA 2.
FT CARBHD 218 218 N-linked (GlcNAc...) (Potential).
FT DISULFD 30 46 By similarity.
FT DISULFD 70 70 By similarity.
SQ SEQUENCE 547 AA; 59427 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. NO. 1.9e-65;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

QY 60 VKCPAGCDDPKYHVTGVYASVSSGAAHVGVLDSGGKILYKVAAGSGVSGSYN 119
DB 44 VLCRANGLMOPFYFGDGIYASLSVSCAHLHRYITAGAAVQVITPGQENTPAVHAN 103
QY 120 GVGSLSLPRWRESFVLESKPKKGVYPSALTYSKSPAAQAGRTTAYORPPIPTTA 179
DB 104 GIGCGFSRWMSSEFV-----TPGTNN 125
QY 180 QPVLMLQALVAVVATPTTIPRSPSAATSTIPRQSVGHRQENDLMSTATTYSQN 239
DB 126 ---LAEAVGRSVATARPAT----- 142
QY 240 RPRADPGIORODPSGAARQKPVGADVSLGLVPEKELESTOSLEPVLSDPPNCKIDSLFD 299
DB 143 -----GKPKKTLLEKKA-----GNKDKADIAFLID 168
QY 300 GSTSIGKRRFRIOQLADVAQALDIGPAGLGMVQYGDPAATHFNLKTHNSRDLKTA 359
DB 229 IKEIGFRRGNSTKALHGAHQKFFSMENGRKGIPIKIIVFLDGMPSDDLEBGIVARE 288
QY 169 GSYNIGRRFNLQKNFVGKAVMLGIGTEGPHVGVQASEHPKIEFLYKNTAKEVLEFA 228
QY 360 IEXTTGGELSNVGRALSFYTKNFFSKANGRSAPNVVVVMDGMPDKKEEKSRLARE 419
DB 229 IKEIGFRRGNSTKALHGAHQKFFSMENGRKGIPIKIIVFLDGMPSDDLEBGIVARE 288
QY 420 SGINIFFTTIGGAENEKQYVVEPNFANKAVCRITNGFSLHVOSEGLHKTLOPLVRCV 479
DB 289 FGVAVFIVSAKPTTEELGMVODIGFDKAVCRNNGFSSYQMPSPFGTTKYKVLVQKLC 348
QY 480 DTDLAASCTGLNSADIGFVIDSSSVGTGNFVTLQFTNLTKFEISDTRIGAVOY 539
DB 349 SHEQMLCSKTCYNVNIGFLIDSSSVGSNFRILMLEFISVAKAFEISDGIATVQF 408
QY 540 TYEGRLGEPFKYSKSDILNAIKRVGVMSGCTGTGAINALQLPKFSKPNRK-LMI 598

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DB 409 TYDQRTFSFTDYTKERKVALRNIRYMSGTATGDAISFTTNVGPVKANGKFLV 468
QY 599 LITGRSYDPRIPAMAHLKGVITVAIGVMAAOEELEVATAPARDHSFVDFDULH 658
DB 469 ILTGGQSYDDVGRVAAVAKRGITVPSGVAMAPLDLKDMAESPRESHTFTFEFGLE 528
QY 659 QYVPRIIQNTCTEF 672
DB 529 QMVDPIRGICKDF 542

RESULT 14
COCH_HUMAN
ID COCH_HUMAN STANDARD; PRT; 550 AA.
AC O43405;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 56.
DE Cochlin precursor (COCH-5B2).
GN Name=COCH; Synonyms=COCH5B2; ORFNames=UNQ257/PRO294;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Cochlea;
RX MEDLINE=98110569; PubMed=9441737; DOI=10.1006/geno.1997.5067;
RA Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R.,
RA Kovatch K.A., Batey J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9."
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chan J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Batton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vages A.,
RA Vandell R.L., Watanabe C., Weiland D., Woods K., Xie M.-H.,
RA Yasuda D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.L., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-135; ASN-281;
RP SER-352 AND VAL-402.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Bettucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-
RT PHRC, Seattle, WA (URL: http://pga.gs.washington.edu)";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBD databases.
RN [4]
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RX MEDLINE=22727166; PubMed=12843317; DOI=10.1136/jmg.40.7.479;
RA Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the sensorineural
RT deafness and vestibular disorder, DFNA9."
RL J. Med. Genet. 40:479-486(2003).
RN [5]
RP STRUCTURE BY NMR OF 27-126.
RX MEDLINE=21458424; PubMed=11574466; DOI=10.1093/emboj/20.19.5347;
RA Ljepush E., Teytler M., Kalkonen A., Weigelt J., Banyai L.,
RA Patthy L., Oetting G.,
RT "NMR structure of the LCCL domain and implications for DFNA9 deafness
RT disorder."

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Db      | 32 ITCTFRGLDIRKEKADVLCGGCPLLEEFSSVGNIVYAVSSICGAARGVATNSGGGVR 91
Qy      | 104 VRKVGOSGKGSYSNGVOSLSLPRMRESFVLESKEPKKGVTPYPSALTYSKSPAAQAG 163
Db      | 92 VYSLRGRENYSVDANG:QSQMLSRMSASFTYTKK-----SSTQATGQA- 137
Qy      | 164 ETTKAYQRPPIPGTTAOPVTLMQLIAVTVAATPTTLPRPSPSAASTTSIPRPOSVGHR 223
Db      | 138 -----VSTAHF----- 143
Qy      | 224 QEMDMSTATYTSQNRPRADPGIORODPSGAAPKPGADVSLGLVPEKEELSTQSLPEV 283
Db      | 144 -----PTGRRLK-----TTEKK----- 156
Qy      | 284 SLGPNCKIDLSFLIDGSTSGKRRFRIOKOLLADVAOALDIGPAPLMGVQYGDNPAT 343
Db      | 157 -TGNDCKADIAFLIDGSFNIGQRFFVLOKXNFVGVALLMIGITGEPHVGVLQASHPKI 215
Qy      | 344 HFNKHTNSRDLKTAIEKITQRGGLSNVGRASIFVTNPFPSKANGSGAPNVVVVMD 403
Db      | 216 EFLYLNFTSAKVDLFAIKVEVFRGNSNTGKALKHTAQKFTVDAGVAKGI PKVVVFID 275
Qy      | 404 GMPDVKVEASRLARESGINIFITIEGAENKQYVEENPANKAVCTRTGFSYLAHQ 463
Db      | 276 GMPSDDIEAGIVAREFGVNFIVSAKPIBELGMQDVTFVDAKVRNNGFFSYHMPN 335
Qy      | 464 WFGHLKTOPLVKRCVCDTDLACSKTCLNSADIGFVIDSSVGNFRNTLOPFTNLTK 523
Db      | 336 WFGTTKYKPLVOKLCTHEQMCMCKTCYNVNIAPFLIDSSSVGDSNRLMLERFVSNIAK 395
Qy      | 524 EFEISDTRIGAVQYTYEORLEFGFDKYSKPDILNAIKVGVWGSSTGAALNFAL 583
Db      | 396 TFEISDIGAKIAAVQFYTDQRTFESFTDYSTKENVLAVIRNIRVMSGTATGDAISFTVR 455
Qy      | 584 QLFK--KSKPKRKMLILTDGRSYDVIRIPMAAHLKGVITTAIGVAAAQEBELVIAT 641
Db      | 456 NVFGIRPSPNK-NFLVITVDGQSYDDVQGPAAAHADAGITIFSVGVAMAPLDLKMAS 514
Qy      | 642 HPARDHSFFVDEFDNLHQVPRRIIONICTEF 672
Db      | 515 KPESHAFTRFETGLEPIVSDVIRIGICRDF 545

RESULT 15
OSEA64_BOVIN PRELIMINARY; PRT; 550 AA.
ID OSEA64_BOVIN
AC OSEA64_T
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Coagulation factor C homolog, coochlin.
GN Name=COCH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled.
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckom C.G.,
RA Petrea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keefe J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled;

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RA Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
RA Snelling W.M., Weidman R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
CC EMBL: BT020705; AA008722.1; -; mRNA.
DR SMR: OSEA64: 29-124.
DR Ensembl: ENSBTAG00000021844; Bos taurus.
DR InterPro: IPR04043; LCCL.
DR InterPro: IPR02035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VWF_A; 2.
SQ SEQUENCE 550 AA; 59594 MW; DB3B21839C68D209 CRC64;

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Query Match 32.1%; Score 1123.5; DB 2; Length 550;
 Best Local Similarity 36.8%; Pred. No. 1.9e-64;
 Matches 232; Conservative 103; Mismatches 177; Indels 119; Gaps 7;

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Qy      | 44 INCVKRGKGIIDPEFIKVCAGCDDPKYHYGTDVNVASVSGVGAHSGVLNDSGGKIL 103
Db      | 32 ITCTFRGLDIRKEADVLCGGCPLLEEFSSVGNIVYAVSSICGAARGVATNSGGGVR 91
Qy      | 104 VRKVGOSGKGSYSNGVOSLSLPRMRESFVLESKEPKKGVTPYPSALTYSKSPAAQAG 163
Db      | 92 VYSLRGRENYSVDANG:QSQMLSRMSASFTYTKK-----SSTQATGQA- 137
Qy      | 164 ETTKAYQRPPIPGTTAOPVTLMQLIAVTVAATPTTLPRPSPSAASTTSIPRPOSVGHR 223
Db      | 138 -----VSTAHF----- 148
Qy      | 224 QEMDMSTATYTSQNRPRADPGIORODPSGAAPKPGADVSLGLVPEKEELSTQSLPEV 283
Db      | 149 -----LKTPEKK----- 156
Qy      | 284 SLGPNCKIDLSFLIDGSTSGKRRFRIOKOLLADVAOALDIGPAPLMGVQYGDNPAT 343
Db      | 157 -TGNDCKADIAFLIDGSFNIGQRFFVLOKXNFVGVALLMIGITGEPHVGVLQASHPKI 215
Qy      | 344 HFNKHTNSRDLKTAIEKITQRGGLSNVGRASIFVTNPFPSKANGSGAPNVVVVMD 403
Db      | 216 EFLYLNFTSAKVDLFAIKVEVFRGNSNTGKALKHTAQKFTVDAGVAKGI PKVVVFID 275
Qy      | 404 GMPDVKVEASRLARESGINIFITIEGAENKQYVEENPANKAVCTRTGFSYLAHQ 463
Db      | 276 GMPSDDIEAGIVAREFGVNFIVSAKPIBELGMQDVTFVDAKVRNNGFFSYHMPN 335
Qy      | 464 WFGHLKTOPLVKRCVCDTDLACSKTCLNSADIGFVIDSSVGNFRNTLOPFTNLTK 523
Db      | 336 WFGTTKYKPLVOKLCTHEQMCMCKTCYNVNIAPFLIDSSSVGDSNRLMLERFVSNIAK 395
Qy      | 524 EFEISDTRIGAVQYTYEORLEFGFDKYSKPDILNAIKVGVWGSSTGAALNFAL 583
Db      | 396 TFEISDIGAKIAAVQFYTDQRTFESFTDYSTKENVLAVIRNIRVMSGTATGDAISFTVR 455
Qy      | 584 QLFK--KSKPKRKMLILTDGRSYDVIRIPMAAHLKGVITTAIGVAAAQEBELVIAT 641
Db      | 456 NVFGIRPSPNK-NFLVITVDGQSYDDVQGPAAAHADAGITIFSVGVAMAPLDLKMAS 514
Qy      | 642 HPARDHSFFVDEFDNLHQVPRRIIONICTEF 672
Db      | 515 KPESHAFTRFETGLEPIVSDVIRIGICRDF 545

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Search completed: September 5, 2006, 20:07:20

Wed Sep 6 10:42:03 2006

us-10-063-538-34.rup.spdi

Page 26

Job time : 370 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 5, 2006, 19:59:38 ; Search time 44 Seconds
(without alignments)
1482.613 Million cell updates/sec

Title: US-10-063-538-34

Perfect score: 3502

Sequence: 1 MRTVLVTKASVIMFLVL.....QYVPRIIIONICTERNQPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	15.8	3124	2 A40020	collagen alpha 1(X
2	504.5	14.4	3137	2 A37797	collagen alpha 3(V
3	501.5	14.3	496	2 A37979	cartilage matrix P
4	490	14.0	493	2 A33809	cartilage matrix P
5	490	14.0	500	2 S65522	cartilage matrix P
6	471.5	13.5	3176	2 CGHJ3A	collagen alpha 3(V
7	331	9.5	1857	2 S31212	collagen alpha 1(X
8	331	9.5	1888	2 S78476	collagen alpha 1(X
9	329.5	9.4	2944	2 A54849	collagen alpha 1(X
10	329	9.4	1747	2 A45974	collagen alpha 1(X
11	314.5	9.0	567	2 T28797	collagen alpha 1(X
12	298	8.5	741	2 T46488	hypothetical prote
13	280.5	8.0	929	2 I51027	type XII collagen
14	279	8.0	3051	2 S42373	hypothetical prote
15	266	7.6	2813	1 VMHU	von Willebrand fac
16	262.5	7.5	843	2 A40970	unulin 1 - human
17	252.5	7.2	1019	1 A32856	collagen alpha 1(V
18	231	6.6	1153	1 RWHU1B	cell surface glyco
19	229	6.5	550	2 T23760	hypothetical prote
20	229	6.5	1153	2 S00551	leukocyte surface
21	228	6.5	1163	1 RWHU1C	cell surface glyco
22	226.5	6.5	427	2 G00039	von Willebrand fac
23	226.5	6.5	1025	2 S34033	collagen alpha 1(V
24	213.5	6.1	414	2 P50323	von Willebrand fac
25	213.5	6.1	1286	2 A68396	protein M01B10.2 f
26	210.5	6.0	2098	2 T18397	protein CTRP - mal
27	209.5	6.0	1022	2 S04111	collagen alpha 2(V
28	209	6.0	918	2 S23377	collagen alpha 2(V
29	205	5.9	1028	1 CGHJ1A	collagen alpha 1(V

30	205	5.9	1029	1 S21369	collagen alpha 2(V
31	204	5.8	13055	2 T16580	hypothetical prote
32	203.5	5.8	1170	2 S03308	cell surface glyco
33	203.5	5.8	1180	2 A35854	integrin alpha-1 c
34	200	5.7	238	2 C35243	collagen alpha 2(V
35	200	5.7	917	2 S09646	collagen alpha 2(V
36	200	5.7	1018	1 CGHJ2A	collagen alpha 2(V
37	195	5.6	1163	2 I56126	lymphocyte fuction
38	193	5.5	1151	2 A45226	integrin alpha-1 c
39	188.5	5.4	272	2 A55348	integrin alpha-1 c
40	187.5	5.4	1170	2 T45914	integrin alpha 2 s
41	184.5	5.3	643	2 T19549	hypothetical prote
42	182.5	5.2	1181	2 A33958	integrin alpha-2 c
43	178	5.1	763	2 I50807	complement factor
44	171	4.9	712	2 A45638	immunodominant mic
45	170.5	4.9	1178	2 S44142	VIA-2 protein homo
46	166.5	4.8	1178	2 T47230	VIA-2 protein - pi
47	162.5	4.6	1179	2 A53213	integrin alpha-E c
48	159.5	4.6	1019	2 A38738	coagulation factor
49	159	4.5	640	2 T29784	hypothetical prote
50	150.5	4.3	724	2 A48569	antigen Em100 - Ei
51	146	4.2	371	2 S32604	collagen alpha 2(V
52	141.5	4.0	2938	2 T30249	cell proliferation
53	140.5	4.0	449	2 T33257	hypothetical prote
54	135.5	3.9	833	2 A62089	hypothetical prote
55	131	3.7	959	2 S32605	collagen alpha 3(V
56	128.5	3.7	341	2 T32949	hypothetical prote
57	128	3.7	1200	2 T17404	hypothetical prote
58	125.5	3.6	474	2 T31064	hyalin - sea urchi
59	125.5	3.6	661	2 T16587	hypothetical prote
60	125	3.6	478	2 T110030	hypothetical prote
61	125	3.6	586	2 H86914	conserved hypotet
62	124.5	3.6	921	2 G02326	transcription fact
63	123.5	3.5	460	2 T23087	hypothetical prote
64	122.5	3.5	1777	2 T34369	hypothetical prote
65	122	3.5	1595	2 T31082	endo-1,4-beta-xyla
66	121.5	3.5	445	2 B40970	undulin 2 - human
67	121.5	3.5	915	2 T09575	smoochelin - human
68	120.5	3.4	2013	2 AD1129	probable peptidogl
69	120	3.4	573	2 A33533	cell surface glyco
70	120	3.4	939	2 AE2275	hypothetical prote
71	119	3.4	725	2 A41258	hypothetical prote
72	119	3.4	1328	2 T43060	agrin - electric r
73	119	3.4	1588	2 A86036	probable adhesin Z
74	119	3.4	1588	2 H91188	cadherin-7 - chick
75	118.5	3.4	785	2 I50180	von Willebrand fac
76	117.5	3.4	780	2 A34102	genome polypeptid
77	116	3.3	2733	2 S15760	threonine ammonia-
78	115	3.3	595	2 A38628	hypothetical prote
79	114	3.3	227	2 T12549	p45 NF-E2 related
80	114	3.3	581	2 I49261	glycerophosphoryl
81	114	3.3	786	2 D75630	Lu-ECM-1 protein
82	114	3.3	905	2 T02205	related to supres
83	114	3.3	1174	2 T49868	hypothetical prote
84	113	3.2	771	2 T34376	transforming prote
85	112.5	3.2	428	1 TVHUEK	signal recognition
86	112.5	3.2	638	2 A24570	hypothetical prote
87	112.5	3.2	1028	2 T34360	hypothetical prote
88	112	3.2	484	2 F83330	RND divalent metal
89	112	3.2	710	2 T44753	hypothetical prote
90	112	3.2	733	2 A87168	conserved hypotet
91	112	3.2	1557	2 T13160	protein CNK - frui
92	112	3.2	1660	2 A84647	hypothetical prote
93	112	3.2	2214	2 T16305	hypothetical prote
94	111.5	3.2	382	2 T14336	RAD23 protein, iso
95	111.5	3.2	385	2 E96669	protein FIN19.19 f
96	110.5	3.2	1066	2 G84746	hypothetical prote
97	110.5	3.2	1081	2 S66736	transcription acti
98	110	3.1	853	2 AC2079	glutathione-iron r
99	110	3.1	1367	1 S48478	flucan 1,4-alpha-g
100	109.5	3.1	667	2 T00061	hypothetical prote
101	109.5	3.1	1809	2 S57329	tuberos sclerosis
102	109	3.1	270	2 E87649	hypothetical prote

103	109	3.1	452	2	T46147	176	101.5	2.9	632	2	D98191	trka-like protein
104	109	3.1	802	2	T21315	177	101.5	2.9	881	2	S56032	probable membrane
105	109	3.1	1091	2	S38850	178	101.5	2.9	932	2	T21338	hypothetical prote
106	108.5	3.1	652	2	T37822	179	101.5	2.9	1093	2	T38533	AF17 protein - hum
107	108.5	3.1	1779	2	T31085	180	101.5	2.9	1335	2	T32021	autolysin E - St
108	108	3.1	402	1	QRB072	181	101.5	2.9	1943	2	B64596	toxin-like outer m
109	108	3.1	511	2	S50114	182	101.5	2.9	2166	2	H89960	hypothetical prote
110	108	3.1	1324	2	S52863	183	101	2.9	497	2	T41015	hypothetical rich
111	108	3.1	1634	2	T26517	184	101	2.9	932	2	T40216	probable histone t
112	107.5	3.1	509	2	AG0365	185	101	2.9	949	2	JC7802	Urb protein - mous
113	107.5	3.1	1200	2	T48194	186	101	2.9	997	2	T15243	hypothetical prote
114	107.5	3.1	1501	2	T45623	187	101	2.9	1575	2	S68448	synproctamin, 170k
115	107	3.1	432	2	UC4864	188	101	2.9	3216	2	C90538	hypothetical prote
116	107	3.1	660	2	JM0057	189	100.5	2.9	433	2	S52974	regulatory protein
117	107	3.1	856	2	C85023	190	100.5	2.9	593	2	D97806	penicillin-binding
118	107	3.1	1450	2	C86880	191	100.5	2.9	645	2	G01205	TYL protein - huma
119	106.5	3.0	721	2	T41555	192	100.5	2.9	769	2	T22316	hypothetical prote
120	106.5	3.0	794	2	T37989	193	100.5	2.9	832	2	T31288	hypothetical prote
121	106.5	3.0	800	2	S29344	194	100.5	2.9	878	1	A40091	interleukin-3 rece
122	106	3.0	351	2	S50754	195	100.5	2.9	1220	2	T19117	hypothetical prote
123	106	3.0	691	2	B75622	196	100.5	2.9	1849	2	C41859	IGA-specific metal
124	106	3.0	963	2	T48707	197	100.5	2.9	2354	2	T13288	mei-41 protein - f
125	106	3.0	1072	2	A37127	198	100	2.9	371	2	F70555	hypothetical prote
126	105.5	3.0	528	2	T52092	199	100	2.9	404	2	T14729	betaine-aldehyde d
127	105.5	3.0	817	2	S51342	200	100	2.9	681	2	T17858	hypothetical Brach
128	105.5	3.0	826	2	A45559	201	100	2.9	718	2	F64628	flagellar hook pro
129	105.5	3.0	1043	2	F97302	202	100	2.9	802	2	B43735	bcsB protein - Ace
130	105.5	3.0	1299	2	T47182	203	100	2.9	873	2	A47283	calphostin - fruit
131	105.5	3.0	1748	1	J01555	204	100	2.9	1006	2	T00050	hypothetical prote
132	105	3.0	367	2	AG3032	205	100	2.9	1045	2	A29840	serine proteinase
133	105	3.0	412	2	E98253	206	100	2.9	1247	2	T45743	hypothetical prote
134	105	3.0	562	1	HMIV2	207	100	2.9	1420	2	T37781	probable cytokele
135	105	3.0	1048	2	A70592	208	100	2.9	2232	2	T34434	hypothetical prote
136	105	3.0	2514	2	F81045	209	99.5	2.8	318	2	E82493	conserved hypotet
137	105	3.0	3005	2	T08841	210	99.5	2.8	436	2	A48399	hypothetical prote
138	104.5	3.0	671	2	T02504	211	99.5	2.8	633	2	AC3534	noD protein (limp
139	104.5	3.0	764	2	S75407	212	99.5	2.8	743	2	T09173	EH domain protein
140	104.5	3.0	880	2	S60137	213	99.5	2.8	1131	2	T41144	hypothetical seirin
141	104.5	3.0	931	2	T49710	214	99.5	2.8	1162	2	T30194	nuclear protein SA
142	104.5	3.0	963	2	T40290	215	99.5	2.8	1196	2	T14108	SH3-containing pro
143	104.5	3.0	2013	2	A11489	216	99.5	2.8	1306	2	S22624	aggregation protei
144	104	3.0	337	1	DEZMGC	217	99.5	2.8	1723	2	H86557	polymorphic membra
145	104	3.0	429	2	UC4965	218	99.5	2.8	1732	2	E72067	polymorphic membra
146	104	3.0	582	2	A70755	219	99.5	2.8	1732	2	C81601	polymorphic membra
147	104	3.0	1091	2	JH0565	220	99.5	2.8	3570	2	T45025	mucin MUC5B, trach
148	104	3.0	1238	2	T34929	221	99.5	2.8	616	2	B33586	C4-dicarboxylate t
149	104	3.0	1679	2	T50091	222	99	2.8	620	2	A70525	hypothetical prote
150	104	3.0	1802	2	S69703	223	99	2.8	621	2	D96032	C4-dicarboxylate t
151	103.5	3.0	575	2	T21775	224	99	2.8	632	2	T02627	hypothetical prote
152	103.5	3.0	656	2	AB1843	225	99	2.8	655	2	E81157	cell division prot
153	103.5	3.0	837	2	A57542	226	99	2.8	660	1	VHWMH2	structural protein
154	103	2.9	349	2	T05857	227	99	2.8	718	2	G71888	flagellar hook pro
155	103	2.9	616	2	T46292	228	99	2.8	750	2	T48804	hypothetical prote
156	103	2.9	719	2	S60771	229	99	2.8	751	2	B87391	TonB-dependent rec
157	103	2.9	803	2	S76106	230	99	2.8	761	1	BBMS	complement factor
158	103	2.9	1566	2	T20058	231	99	2.8	766	2	AS6394	pyocin S3 - Pseudo
159	102.5	2.9	256	2	A60533	232	99	2.8	809	2	H87455	TonB-dependent rec
160	102.5	2.9	425	2	T18723	233	99	2.8	839	2	F75618	hypothetical prote
161	102.5	2.9	465	2	C70594	234	99	2.8	874	2	JC4930	S-layer protein pr
162	102.5	2.9	889	2	A35679	235	99	2.8	1198	2	B88279	protein C08H9.2 [1
163	102.5	2.9	1054	2	S54473	236	99	2.8	1217	2	T39427	probable myosin I
164	102	2.9	353	2	A41558	237	99	2.8	1283	2	T39174	hypothetical Serin
165	102	2.9	392	2	T04150	238	99	2.8	1591	2	AS4146	invasion-inducing
166	102	2.9	719	2	T33170	239	99	2.8	1704	2	A55426	gingipain R (EC 3.
167	102	2.9	776	2	AB0998	240	99	2.8	1744	1	CAHU	complement C4a pre
168	102	2.9	1008	2	T12532	241	99	2.8	1764	2	T15171	hypothetical prote
169	102	2.9	1341	2	S09579	242	98.5	2.8	252	2	T04739	hypothetical prote
170	102	2.9	2229	2	T16199	243	98.5	2.8	329	2	S17765	major storage prot
171	102	2.9	2441	2	S39161	244	98.5	2.8	564	2	AF2351	serine/threonine k
172	101.5	2.9	328	2	C42756	245	98.5	2.8	654	2	T33044	hypothetical prote
173	101.5	2.9	574	2	F75356	246	98.5	2.8	662	2	I36400	melanoma-associate
174	101.5	2.9	631	2	D95348	247	98.5	2.8	668	2	A41234	melanocyte-specific
175	101.5	2.9	632	2	AF3095	248	98.5	2.8	746	2	T46821	sideophore recep

249	98.5	2.8	746	2	A95420	RhA Rhizobactin r	322	96.5	2.8	1219	2	T14578	nucleoporin Nup153
250	98.5	2.8	790	2	T47959	hypothetical prote	323	96.5	2.8	1433	2	A71444	probable LTR retro
251	98.5	2.8	970	2	F87450	Tomb-dependent rec	324	96.5	2.8	2823	2	F87908	protein T22a-8 (i
252	98.5	2.8	1043	2	T19734	hypothetical prote	325	96.5	2.8	2823	2	T23064	hypothetical prote
253	98.5	2.8	1232	2	S40766	hypothetical prote	326	96.5	2.8	3102	2	T43291	laminin alpha chain
254	98.5	2.8	2298	2	T49648	hypothetical prote	327	96.5	2.8	3144	2	A46068	Huntington disease
255	98	2.8	294	2	A37232	mucin, tracheal (A	328	96	2.7	273	2	A84332	hypothetical prote
256	98	2.8	376	2	T20972	hypothetical prote	329	96	2.7	327	2	E70180	hypothetical prote
257	98	2.8	438	2	B69023	conserved hypotet	330	96	2.7	450	2	T17234	hypothetical prote
258	98	2.8	460	2	T45968	hypothetical prote	331	96	2.7	510	2	H84824	hypothetical prote
259	98	2.8	543	2	S56830	probable purine nu	332	96	2.7	559	2	S60473	En/Spm-like transp
260	98	2.8	559	2	S04531	thrombospondin-rel	333	96	2.7	583	2	T12574	phosphoglycerate m
261	98	2.8	581	2	S63183	CNN1 protein - yea	334	96	2.7	613	2	T36922	probable large sec
262	98	2.8	635	2	E81948	probable ATP-depen	335	96	2.7	705	2	T31261	hypothetical prote
263	98	2.8	726	2	T40790	probable permease	336	96	2.7	716	2	T26998	hypothetical prote
264	98	2.8	1020	2	T29108	hypothetical prote	337	96	2.7	740	1	B65136	YnfF protein - Bac
265	98	2.8	1088	1	IXJLNL	neural cell adhesi	338	96	2.7	740	2	H86005	hypothetical prote
266	98	2.8	1106	1	CHRA2	calcium channel pr	339	96	2.7	740	2	A98160	hypothetical prote
267	98	2.8	1291	2	S44983	vacuolating cyto	340	96	2.7	781	2	T41551	L66 protein - Yip
268	98	2.8	2440	2	S39162	transcriptional coc	341	96	2.7	867	2	JH0225	probable Myb-famil
269	97.5	2.8	340	2	B83262	hypothetical prote	342	96	2.7	873	2	F96615	ciathrin assembly
270	97.5	2.8	359	2	S42787	serine/threonine-r	343	96	2.7	896	2	S36326	auxilin - bovine
271	97.5	2.8	412	2	T35514	probable glycosyl	344	96	2.7	910	2	S68983	auxilin - bovine
272	97.5	2.8	499	2	S09880	hypothetical prote	345	96	2.7	946	2	JC5575	inter-alpha-lypsi
273	97.5	2.8	568	2	UC7317	cyclin-dependent k	346	96	2.7	1076	2	A35622	nuclear pore prote
274	97.5	2.8	670	2	T00083	hypothetical prote	347	96	2.7	1125	2	B41206	microtubule-associ
275	97.5	2.8	686	2	A38235	microtubule-associ	348	96	2.7	1392	2	A43336	microtubule-vesicl
276	97.5	2.8	823	2	A36378	probable transcrip	349	96	2.7	1456	2	S14005	hypothetical prote
277	97.5	2.8	882	2	B96931	hypothetical prote	350	96	2.7	3421	1	WZBE86	367K tegument prot
278	97.5	2.8	882	2	AC2082	feric aerobactin	351	95.5	2.7	316	2	T34553	hypothetical prote
279	97.5	2.8	916	2	F97033	penicillin-binding	352	95.5	2.7	391	2	E84392	aspartate aminotra
280	97.5	2.8	926	2	T48391	protein kinase-Iik	353	95.5	2.7	462	1	QOBE94	HRF4 protein - hu
281	97.5	2.8	1129	2	S52631	phytochrome A - pa	354	95.5	2.7	521	2	C96700	protein P12A21.15
282	97.5	2.8	1288	2	E71884	vacuolating cyto	355	95.5	2.7	526	2	A56573	nuclear pore compl
283	97.5	2.8	1711	2	AB1283	peptidoglycan link	356	95.5	2.7	566	2	H82132	long-chain-fatty-a
284	97.5	2.8	1879	2	S74915	extracellular nuci	357	95.5	2.7	635	2	F75477	hypothetical prote
285	97.5	2.8	2187	2	T30826	nascent polypeptid	358	95.5	2.7	653	2	JQ1241	Viral replicase 1
286	97.5	2.8	2311	1	TVCHSR	kinase-related pro	359	95.5	2.7	1039	2	S02711	cellulase (EC 3.2.
287	97.5	2.8	2957	2	T33152	hypothetical prote	360	95.5	2.7	1177	1	S66085	transcription-repa
288	97	2.8	407	2	I52703	42k membrane glyco	361	95.5	2.7	1287	2	B53739	vacuolating cyto
289	97	2.8	472	2	I67793	microtubule-associ	362	95.5	2.7	1568	2	T09074	semaphorin recepto
290	97	2.8	623	2	A48123	cell cycle regulat	363	95.5	2.7	1762	2	T03222	probable polyketid
291	97	2.8	677	2	JC7303	pectate lyase (EC	364	95.5	2.7	1794	2	T38459	hypothetical diver
292	97	2.8	758	1	SUECCA	ATP-binding compon	365	95	2.7	2225	1	A23443	pyridine synthe
293	97	2.8	758	2	H90749	ATP-binding compon	366	95	2.7	417	2	A12003	hypothetical prote
294	97	2.8	758	2	D85600	cell division prot	367	95	2.7	472	2	T24618	hypothetical prote
295	97	2.8	806	2	F72024	cell division prot	368	95	2.7	518	1	XYIMHA	homoserine O-acety
296	97	2.8	806	2	F86600	autotransporter pr	369	95	2.7	536	2	B83278	probable aminopept
297	97	2.8	868	2	AF3204	DNA-directed RNA p	370	95	2.7	544	2	H72647	hypothetical prote
298	97	2.8	870	2	F69406	conserved hypotet	371	95	2.7	597	1	S43743	probable dual spec
299	97	2.8	881	2	F69438	hypothetical prote	372	95	2.7	641	2	JC6017	zinc-finger trans
300	97	2.8	896	2	T22061	phosphoprotein, sy	373	95	2.7	676	1	S69783	outer membrane pro
301	97	2.8	901	2	A44825	carbamoyl-phosphat	374	95	2.7	742	2	AH2166	hypothetical prote
302	97	2.8	1162	2	AD3317	subunit A of ATP-d	375	95	2.7	747	2	T39744	conserved hypotet
303	97	2.8	1203	2	DB6625	exopolysaccharona	376	95	2.7	824	2	T36818	probable secreted
304	97	2.8	1376	2	F83711	tuberos scleriosis	377	95	2.7	824	2	A47282	calcium-binding pr
305	97	2.8	1784	2	A49420	hypothetical prote	378	95	2.7	872	2	AC2134	ferriochrome-iron r
306	96.5	2.8	409	2	T18726	serine proteinase	379	95	2.7	886	2	S29605	glycoprotein 350/2
307	96.5	2.8	533	1	JU0146	probable membrane	380	95	2.7	916	2	G97053	penicillin-binding
308	96.5	2.8	542	2	S64030	probable signal tr	381	95	2.7	1025	2	S69790	fibronectin-bindin
309	96.5	2.8	670	2	S67383	P09G8.8 protein -	382	95	2.7	1063	2	T00624	endo-1,4-beta-xyla
310	96.5	2.8	746	2	S44792	complement factor	383	95	2.7	1092	2	T33717	carbamoyl-phosphat
311	96.5	2.8	764	1	BBHU	beta-xylosidase-li	384	95	2.7	1184	2	S50832	alpha, alpha-trehal
312	96.5	2.8	773	2	T49925	hypothetical prote	385	95	2.7	1184	2	S50832	atrophin-1 - human
313	96.5	2.8	803	2	T18738	probable adenylate	386	95	2.7	1184	2	G01763	atrophin-1 - human
314	96.5	2.8	829	2	D71485	cell surface glyco	387	95	2.7	1785	2	A45546	major mezozoite su
315	96.5	2.8	867	2	B84417	hypothetical prote	388	95	2.7	4548	1	S00657	apoptrotein(a) (EC
316	96.5	2.8	867	2	AD1856	hypothetical prote	389	95	2.7	13288	2	T03099	mucin, submaxillar
317	96.5	2.8	918	2	T02759	hypothetical prote	390	94.5	2.7	473	2	B36963	bcsA 5'-region pro
318	96.5	2.8	1013	2	B75583	hypothetical prote	391	94.5	2.7	473	2	T10271	capsid-associated
319	96.5	2.8	1032	2	T34433	transcription fact	392	94.5	2.7	502	2	G87433	conserved hypotet
320	96.5	2.8	1037	2	T33350	high molecular mas	393	94.5	2.7	530	2	S62439	hypothetical serin
321	96.5	2.8	1151	2	T18535		394	94.5	2.7	538	2	I59291	beta1-syntrophin -

395	94.5	2.7	699	2	C43674	468	93	2.7	1526	2	S49763	gingipain R (EC 3.
396	94.5	2.7	704	2	A30411	469	93	2.7	1611	2	T38236	hypothetical prote
397	94.5	2.7	705	2	H89900	470	93	2.7	1792	2	A57075	tensin - chicken (
398	94.5	2.7	734	2	S44617	471	93	2.7	1820	2	A55494	latent transformin
399	94.5	2.7	856	2	T43631	472	93	2.7	2468	2	A83412	hypothetical prote
400	94.5	2.7	875	2	T12794	473	93	2.7	3433	1	GNNYKV	genome polypeptide
401	94.5	2.7	876	1	A57988	474	93	2.7	4688	2	F82885	hypothetical prote
402	94.5	2.7	913	2	S20590	475	92.5	2.6	487	2	D64551	outer membrane pro
403	94.5	2.7	924	2	A44945	476	92.5	2.6	508	2	A32225	nerve growth facto
404	94.5	2.7	1185	2	T19212	477	92.5	2.6	563	2	J00623	gamma-glutamyltran
405	94.5	2.7	1282	2	JC4393	478	92.5	2.6	581	2	E91165	gamma-glutamyltran
406	94.5	2.7	1306	2	S25370	479	92.5	2.6	581	2	E86011	gamma-glutamyltran
407	94.5	2.7	1487	1	EDBE81	480	92.5	2.6	639	2	E98281	cobr protein (impo
408	94.5	2.7	3104	2	S20473	481	92.5	2.6	639	2	AC3002	cobryntic acid syn
409	94.5	2.7	3890	2	C89921	482	92.5	2.6	662	2	T51948	omnipotent nonsens
410	94	2.7	403	2	C70832	483	92.5	2.6	756	2	G64150	P22M8.3 protein -
411	94	2.7	483	2	F83205	484	92.5	2.6	772	2	S62481	hypothetical prote
412	94	2.7	509	1	O4RT0	485	92.5	2.6	779	2	A57177	NIMA-like protein
413	94	2.7	642	2	T39607	486	92.5	2.6	784	2	S26538	SPR-1 protein - nu
414	94	2.7	649	1	B37953	487	92.5	2.6	860	2	UC4566	chitinase (EC 3.2.
415	94	2.7	678	2	G65104	488	92.5	2.6	946	2	S27921	nuclear antigen Eb
416	94	2.7	754	2	T14877	489	92.5	2.6	1023	2	JC4013	major acidic nucle
417	94	2.7	774	2	D97527	490	92.5	2.6	1238	2	T40120	C2H2 type zinc fin
418	94	2.7	774	2	AE2746	491	92.5	2.6	1325	2	S16429	dynein-associated
419	94	2.7	903	2	T26743	492	92.5	2.6	1844	2	S01956	hypothetical prote
420	94	2.7	928	2	E84483	493	92.5	2.6	1985	2	S19151	hypothetical prote
421	94	2.7	948	2	T11678	494	92.5	2.6	2357	2	A59249	class VII unconven
422	94	2.7	951	2	T26738	495	92.5	2.6	2588	2	T14342	NSD1 protein - mou
423	94	2.7	975	2	T26737	496	92.5	2.6	3083	2	AH2493	hypothetical prote
424	94	2.7	1080	2	S48944	497	92.5	2.6	3924	2	S37431	ankyrin 2, neuron
425	94	2.7	1163	2	D82202	498	92	2.6	270	2	AH2435	hypothetical prote
426	94	2.7	1225	2	T48251	499	92	2.6	427	2	A53798	58k membrane-asso
427	94	2.7	1262	1	B48758	500	92	2.6	509	2	S47553	cytochrome P450 Cy
428	94	2.7	1496	1	A48758	501	92	2.6	540	1	FOWVHL	gag polyprotein -
429	94	2.7	1520	2	AF3008	502	92	2.6	550	2	G70597	probable proteinas
430	94	2.7	1520	2	G98275	503	92	2.6	561	2	T14792	hypothetical prote
431	94	2.7	1547	2	T28657	504	92	2.6	567	2	S76847	phosphoglucomutase
432	94	2.7	1578	2	AD1512	505	92	2.6	591	1	S30145	ketol-acid reducto
433	93.5	2.7	580	1	EKECEX	506	92	2.6	591	1	T45681	ketol-acid reducto
434	93.5	2.7	638	2	A29440	507	92	2.6	681	2	A45705	type I transmembra
435	93.5	2.7	666	2	B70803	508	92	2.6	712	2	G02512	interleukin-1 rece
436	93.5	2.7	681	2	F85062	509	92	2.6	747	2	T23507	hypothetical prote
437	93.5	2.7	839	1	GNNIS2	510	92	2.6	784	2	AF1638	DNA translocase ho
438	93.5	2.7	841	2	E71808	511	92	2.6	880	2	AF2128	hypothetical prote
439	93.5	2.7	918	2	C84720	512	92	2.6	907	1	QOBR21	membrane antigen g
440	93.5	2.7	924	2	H85354	513	92	2.6	937	2	T40723	c-1-tetrahydrofol
441	93.5	2.7	981	1	FOWMGM	514	92	2.6	946	2	S54354	inter-alpha-inhibi
442	93.5	2.7	1116	1	B88612	515	92	2.6	1046	2	S67786	hypothetical prote
443	93.5	2.7	1238	1	UC5573	516	92	2.6	1092	2	T18305	replication factor
444	93.5	2.7	1487	1	EDBE6	517	92	2.6	1092	2	T18306	replication factor
445	93.5	2.7	1616	2	T17884	518	92	2.6	1123	2	S20497	phytochrome A - po
446	93.5	2.7	2274	2	T30258	519	92	2.6	1124	1	FKPUZ	phytochrome - zuc
447	93.5	2.7	2731	1	VF1HJH	520	92	2.6	1135	2	T30561	Scythe protein - A
448	93.5	2.7	4735	2	T17463	521	92	2.6	1208	2	S17286	period clock prote
449	93	2.7	260	2	C83362	522	92	2.6	1224	2	T14007	microtubule-associ
450	93	2.7	302	2	D85253	523	92	2.6	1231	2	T30841	serine-repeat anti
451	93	2.7	432	2	JS0306	524	92	2.6	1237	2	A54080	protein-tyrosine-p
452	93	2.7	504	2	AG2373	525	92	2.6	1336	2	S36851	L-shaped tail fibe
453	93	2.7	533	2	JS0304	526	92	2.6	1788	2	AH1447	probable tape-meas
454	93	2.7	574	2	A46283	527	92	2.6	2136	2	B84651	hypothetical prote
455	93	2.7	627	1	UC6534	528	92	2.6	2254	2	D86215	hypothetical prote
456	93	2.7	675	2	E83075	529	92	2.6	2843	1	RBH0AP	adenomatous polypo
457	93	2.7	767	2	A82882	530	92	2.6	3449	2	T01083	hypothetical prote
458	93	2.7	775	2	I49759	531	92	2.6	3507	2	T34513	hypothetical prote
459	93	2.7	836	2	S49940	532	92	2.6	249	2	T21083	hypothetical prote
460	93	2.7	917	2	B85057	533	91.5	2.6	258	2	H75349	hypothetical prote
461	93	2.7	953	2	T12577	534	91.5	2.6	279	2	S53363	uv excision repair
462	93	2.7	973	2	T18341	535	91.5	2.6	368	2	T40115	uv excision repair
463	93	2.7	1159	1	A44280	536	91.5	2.6	374	2	C97965	conserved phospho
464	93	2.7	1234	2	C97606	537	91.5	2.6	468	2	D87004	probable phosphoma
465	93	2.7	1234	2	AE2828	538	91.5	2.6	474	2	E83392	probable transcrip
466	93	2.7	1278	2	T27925	539	91.5	2.6	479	2	G71957	probable outer mem
467	93	2.7	1390	2	T31353	540	91.5	2.6	542	2	I39540	chitinase (EC 3.2.

541	91.5	2.6	562	2	S38145	614	90.5	2.6	466	2	AF0224	Flagellar hook-ass
542	91.5	2.6	627	2	S68958	615	90.5	2.6	472	2	T48074	hypothetical prote
543	91.5	2.6	639	2	S20139	616	90.5	2.6	526	2	C84223	methionyl-CoA
544	91.5	2.6	653	2	E84682	617	90.5	2.6	566	1	HMIIVD8	hemagglutinin prec
545	91.5	2.6	674	2	A97490	618	90.5	2.6	571	2	T43456	hypothetical prote
546	91.5	2.6	703	2	T41065	619	90.5	2.6	580	2	AB0994	gamma-glutamyltran
547	91.5	2.6	793	2	S59067	620	90.5	2.6	600	2	E53290	oligopeptide trans
548	91.5	2.6	852	2	A28459	621	90.5	2.6	642	1	HHBYA1	dhak-type molecula
549	91.5	2.6	863	2	A12077	622	90.5	2.6	645	2	T41372	hypothetical RNA-b
550	91.5	2.6	943	2	T16768	623	90.5	2.6	654	2	T41584	hypothetical prote
551	91.5	2.6	957	2	S32903	624	90.5	2.6	671	2	AC1407	transketolase homo
552	91.5	2.6	1052	2	T14343	625	90.5	2.6	782	2	S27833	iron(III) dicitrat
553	91.5	2.6	1079	2	T10996	626	90.5	2.6	847	2	C97678	FeMB-dependent rec
554	91.5	2.6	1104	2	S59130	627	90.5	2.6	867	2	T45463	membrane glycoprot
555	91.5	2.6	1290	2	G64630	628	90.5	2.6	892	2	T09071	SH3 domains-contai
556	91.5	2.6	1323	2	T30253	629	90.5	2.6	934	2	E64235	hypothetical prote
557	91.5	2.6	1355	2	T00075	630	90.5	2.6	936	2	T23393	hypothetical prote
558	91.5	2.6	1355	2	T00075	631	90.5	2.6	991	2	H86168	hypothetical prote
559	91.5	2.6	1433	2	T30261	632	90.5	2.6	1029	2	A57377	hypothetical prote
560	91.5	2.6	1751	2	A45604	633	90.5	2.6	1075	2	AS7377	transcription fact
561	91.5	2.6	1993	2	AF1450	634	90.5	2.6	1075	2	AS7377	ceramoyl-phosphat
562	91.5	2.6	2109	1	I50421	635	90.5	2.6	1083	2	S59780	hypothetical prote
563	91.5	2.6	2124	2	A28452	636	90.5	2.6	1183	2	S63046	hypothetical prote
564	91.5	2.6	3263	2	E82410	637	90.5	2.6	1234	2	T30160	hypothetical prote
565	91.5	2.6	3562	2	AA7171	638	90.5	2.6	1250	2	T27706	hypothetical prote
566	91	2.6	168	2	G89026	639	90.5	2.6	1357	2	T29265	hypothetical prote
567	91	2.6	338	2	B64336	640	90.5	2.6	1357	2	T29265	hypothetical prote
568	91	2.6	350	2	AD0466	641	90.5	2.6	1466	2	AE1449	hypothetical prote
569	91	2.6	374	2	S46254	642	90.5	2.6	1946	2	AB1180	probable peptidogl
570	91	2.6	452	2	S75956	643	90.5	2.6	2044	2	E70522	probable polyketid
571	91	2.6	488	2	T09138	644	90.5	2.6	2126	2	A48205	All-1 protein +GRE
572	91	2.6	503	2	T39375	645	90.5	2.6	3869	2	A48205	hypothetical prote
573	91	2.6	524	2	AG1455	646	90.5	2.6	340	2	J00431	hypothetical 35.5K
574	91	2.6	524	2	AH1091	647	90	2.6	348	2	J00431	conserved hypotnet
575	91	2.6	530	2	T32812	648	90	2.6	356	2	D82643	microtubule-associ
576	91	2.6	539	2	G72593	649	90	2.6	364	2	A28820	exopolysphatase
577	91	2.6	559	2	B56791	650	90	2.6	397	2	S46691	probable cdc2-like
578	91	2.6	583	2	S67571	651	90	2.6	414	2	T09589	hypothetical prote
579	91	2.6	600	2	T39516	652	90	2.6	428	2	S61623	hypothetical prote
580	91	2.6	627	2	AE1818	653	90	2.6	473	2	S50755	hypothetical prote
581	91	2.6	650	2	T04487	654	90	2.6	491	2	F95010	ABC transporter, B
582	91	2.6	655	1	A55726	655	90	2.6	498	2	S45567	nuclear factor I-A
583	91	2.6	678	2	D91132	656	90	2.6	509	2	S45565	nuclear factor I-A
584	91	2.6	678	2	G85977	657	90	2.6	514	2	C97882	hypothetical prote
585	91	2.6	783	2	E97340	658	90	2.6	551	2	C84721	hypothetical prote
586	91	2.6	791	2	AC0017	659	90	2.6	566	1	HMIIVT8	hemagglutinin prec
587	91	2.6	847	2	F96531	660	90	2.6	580	2	F84471	hypothetical prote
588	91	2.6	896	2	G96946	661	90	2.6	593	2	A96783	unknown protein F2
589	91	2.6	952	2	S50752	662	90	2.6	600	2	T06292	hypothetical prote
590	91	2.6	983	2	F86160	663	90	2.6	610	2	PN0012	mucin 4, tracheal
591	91	2.6	1039	2	A12284	664	90	2.6	658	2	A86231	hypothetical prote
592	91	2.6	1152	2	A33183	665	90	2.6	675	2	D65083	myrelin-lipoprotein
593	91	2.6	1204	2	B83566	666	90	2.6	677	2	JS0178	protein kinase YKR
594	91	2.6	1226	1	S65593	667	90	2.6	799	2	C82929	ATP synthase alpha
595	91	2.6	1260	2	S60896	668	90	2.6	838	2	T08423	Axin homolog Axil
596	91	2.6	1268	2	S33411	669	90	2.6	905	2	T38314	probable vacuolar
597	91	2.6	1275	2	T33369	670	90	2.6	949	1	PXMUP1	H+-exporting ATPas
598	91	2.6	1307	2	T30887	671	90	2.6	1018	2	T40253	hypothetical prote
599	91	2.6	1456	1	MMKGPV	672	90	2.6	1049	2	C95883	probable efflux pr
600	91	2.6	1473	2	A35186	673	90	2.6	1098	2	T08599	probable transcrip
601	91	2.6	1553	2	T03301	674	90	2.6	1164	2	T03814	tumor suppressor p
602	91	2.6	1662	2	T18540	675	90	2.6	1426	2	E90456	oxydoreductase, pr
603	91	2.6	1684	2	H96597	676	90	2.6	1532	2	T39371	transcription regu
604	91	2.6	2090	2	S26058	677	90	2.6	1545	2	T44824	probable membrane
605	91	2.6	2466	2	I67629	678	90	2.6	1589	2	T42233	submaxillary mucin
606	91	2.6	2688	2	I49477	679	90	2.6	1692	2	G01449	probable mucin G2
607	91	2.6	3436	2	D71917	680	90	2.6	1832	2	T31113	mucin-like glycopr
608	91	2.6	3436	2	S55659	681	90	2.6	1994	2	D86452	protein F6N18.13 [
609	90.5	2.6	3436	2	AD2470	682	90	2.6	2500	1	MMHUB2	HIV-BP2 enhancer-b
610	90.5	2.6	316	2	AB1710	683	90	2.6	2559	2	T09144	probable guanine n
611	90.5	2.6	351	2	G84128	684	90	2.6	3034	2	T14119	seven-pass transme
612	90.5	2.6	399	2	T18853	685	90	2.6	4006	2	T09070	probable tenascin
613	90.5	2.6	435	2	G69404	686	90	2.6	5291	2	F90696	hypothetical prote

687	89.5	2.6	336	2	AH0201	probable zinc-bind	760	89	2.5	1159	2	S62562	probable nuclear p
688	89.5	2.6	364	2	T24153	hypothetical prote	761	89	2.5	1164	2	S46769	hypothetical prote
689	89.5	2.6	397	2	T40539	zinc finger protei	762	89	2.5	1194	2	E96624	hypothetical prote
690	89.5	2.6	409	2	A70932	probable PPE prote	763	89	2.5	1224	2	T40765	webl proteoin homol
691	89.5	2.6	420	2	S76691	hypothetical prote	764	89	2.5	1234	2	T31623	hypothetical prote
692	89.5	2.6	428	2	G81352	3-phosphoshikimate	765	89	2.5	1257	2	S28764	neurocan precursor
693	89.5	2.6	435	2	C70456	homoserine dehydro	766	89	2.5	1372	2	T29309	hypothetical prote
694	89.5	2.6	482	2	T36045	hypothetical prote	767	89	2.5	1445	2	A59437	hypothetical prote
695	89.5	2.6	522	2	S41819	nucliosporin p62 -	768	89	2.5	1643	2	T07961	myosin heavy chain
696	89.5	2.6	532	2	S74453	hypothetical prote	769	89	2.5	1737	2	A59235	unconventional myo
697	89.5	2.6	539	2	D82765	N-acetylmutamoyl-L	770	89	2.5	1823	2	S28974	vitellogenin precu
698	89.5	2.6	586	2	T29669	hypothetical prote	771	89	2.5	1859	2	A34092	DNA-directed RNA p
699	89.5	2.6	594	1	D55514	hypothetical prote	772	89	2.5	1862	2	T29959	DNA-directed RNA p
700	89.5	2.6	594	2	C71661	penicillin-binding d	773	89	2.5	2344	1	RRWNRH	genome polyprotein
701	89.5	2.6	636	2	I48718	poly(A) binding pr	774	89	2.5	2344	2	S55399	genome polyprotein
702	89.5	2.6	648	1	P3BP66	P3 protein - phage	775	89	2.5	2649	2	T51023	hypothetical prote
703	89.5	2.6	660	2	T03038	probable inhibitor	776	89	2.5	3020	2	A43932	mucin 2 precursor,
704	89.5	2.6	712	2	B87683	TonB-dependent rec	777	89	2.5	3624	2	AD0835	large repetitive p
705	89.5	2.6	728	2	T38220	hypothetical prote	778	89	2.5	4543	1	A53102	alpha-2-macroglobu
706	89.5	2.6	760	2	AB2225	hypothetical prote	779	89	2.5	4957	2	T03455	ALR protein - huma
707	89.5	2.6	761	2	T41304	probable rna-bindi	780	89	2.5	5188	2	B85547	probable RTX fam1
708	89.5	2.6	766	2	T11650	sak1 protein - fis	781	89	2.5	5262	2	T03454	ALR protein - huma
709	89.5	2.6	779	1	S40382	box A-binding fact	782	88.5	2.5	399	2	G83891	spore germination
710	89.5	2.6	790	2	T34293	hypothetical prote	783	88.5	2.5	443	2	T48708	hypothetical prote
711	89.5	2.6	837	2	T00355	hypothetical prote	784	88.5	2.5	457	2	H85013	hypothetical prote
712	89.5	2.6	866	2	S74291	cytokine receptor	785	88.5	2.5	473	2	E72715	probable aspartate
713	89.5	2.6	896	1	A35782	hypothetical prote	786	88.5	2.5	476	2	G90512	p60-like (mycoplas
714	89.5	2.6	901	2	A49227	salalidase - Actino	787	88.5	2.5	532	2	B35621	spore germination
715	89.5	2.6	924	2	T25007	hypothetical prote	788	88.5	2.5	532	2	AE1964	DNA-type molecula
716	89.5	2.6	927	2	T24031	hypothetical prote	789	88.5	2.5	558	2	G96522	spore germination
717	89.5	2.6	975	1	A28174	methylesterhydr	790	88.5	2.5	674	2	B71438	hypothetical prote
718	89.5	2.6	982	2	A53253	microtubule-associ	791	88.5	2.5	721	2	D82934	ATP-dependent zinc
719	89.5	2.6	993	2	C90072	hypothetical prote	792	88.5	2.5	748	2	T04011	hypothetical prote
720	89.5	2.6	1008	2	T41244	SEC14 protein homo	793	88.5	2.5	771	2	A54273	glucocorticoid rec
721	89.5	2.6	1050	2	S25363	translation elonga	794	88.5	2.5	797	1	VEBEX1	glycoprotein x pre
722	89.5	2.6	1051	2	T51904	hypothetical prote	795	88.5	2.5	800	2	AE3151	glucamylase (lipo
723	89.5	2.6	1058	2	A38564	ubiquitin-protein	796	88.5	2.5	819	2	A53714	protein kinase (EC
724	89.5	2.6	1208	2	T09049	competence factor	797	88.5	2.5	837	2	AB3383	hypothetical membr
725	89.5	2.6	1261	2	S75130	sensory transducti	798	88.5	2.5	861	2	S77409	hypothetical prote
726	89.5	2.6	1298	1	EDBE75	immediate-early pr	799	88.5	2.5	885	1	S26723	DNA-directed RNA p
727	89.5	2.6	1460	2	T00095	hypothetical prote	800	88.5	2.5	954	2	T19765	hypothetical prote
728	89.5	2.6	1463	2	T30193	nuclear receptor c	801	88.5	2.5	976	2	G87389	TonB-dependent rec
729	89.5	2.6	1530	2	AD1663	glutamate synthase	802	88.5	2.5	1014	2	A55260	cytotoxic necrotiz
730	89.5	2.6	1544	2	T04464	hypothetical prote	803	88.5	2.5	1021	2	T05108	hypothetical prote
731	89.5	2.6	1734	2	A54602	microtubule-associ	804	88.5	2.5	1073	1	T08828	plasmid replicatio
732	89.5	2.6	2475	2	S35307	polyprotein pp220	805	88.5	2.5	1166	2	T29099	reverse gyrase - S
733	89.5	2.6	2606	2	T03159	large tegument pro	806	88.5	2.5	1274	2	S55050	cardiac myosin-bin
734	89.5	2.6	3283	2	AC1018	large repetitive p	807	88.5	2.5	1293	2	T30871	orsellinic acid sy
735	89.5	2.6	7463	2	T36248	CNA peptide synthe	808	88.5	2.5	1475	2	S42718	nuclear pore compl
736	89	2.5	261	2	A83829	thiamin biosynthes	809	88.5	2.5	1778	2	AF1116	internalin protein
737	89	2.5	336	2	F95044	FMN-dependent dehy	810	88.5	2.5	1844	1	RRWPTM	genome polyprotein
738	89	2.5	336	2	E97914	isopentenyl diphos	811	88.5	2.5	2251	2	T24490	hypothetical prote
739	89	2.5	376	2	G70301	N-acetylornithine	812	88.5	2.5	2761	2	T21064	hypothetical prote
740	89	2.5	524	2	D82944	hypothetical membr	813	88.5	2.5	2783	1	A41948	alpha-fetoprotein
741	89	2.5	539	2	H72422	hypothetical prote	814	88.5	2.5	3282	2	E82750	hemagglutinin-like
742	89	2.5	546	2	G64803	phosphoglucumutase	815	88.5	2.5	3442	2	B82589	hemagglutinin-like
743	89	2.5	559	2	A42807	phosphoglycerate m	816	88.5	2.5	3455	2	B82519	hemagglutinin-like
744	89	2.5	560	2	D30930	flagellar basal bo	817	88.5	2.5	4385	2	T29042	hypothetical prote
745	89	2.5	593	2	T38547	probable cell divi	818	88.5	2.5	5147	1	IJFFTM	cadherin-related t
746	89	2.5	609	1	A48070	heat shock transcr	819	88.5	2.5	5825	2	T12117	polyporein - fava
747	89	2.5	651	2	E86242	hypothetical prote	820	88	2.5	329	2	S31580	storage protein, b
748	89	2.5	688	2	T18263	S-layer protein -	821	88	2.5	341	2	B28820	microtubule-associ
749	89	2.5	733	2	A45301	microtubule-associ	822	88	2.5	369	2	G83434	translocation prot
750	89	2.5	770	2	T22808	hypothetical prote	823	88	2.5	381	2	T52434	cellulohydrolase
751	89	2.5	862	2	S53913	FKB2 protein - Yea	824	88	2.5	459	2	JC7931	hypothetical prote
752	89	2.5	865	1	S02196	DNA-directed RNA p	825	88	2.5	465	2	G90961	flagellar capping
753	89	2.5	878	2	T21621	hypothetical prote	826	88	2.5	465	2	G85809	flagellar capping
754	89	2.5	927	2	F82818	conserved hypochet	827	88	2.5	468	2	A64956	flagellar hook-ass
755	89	2.5	929	2	T35683	ftsK homolog - Str	828	88	2.5	466	2	T49017	hypothetical prote
756	89	2.5	976	2	A85756	peptidase, M16 fam	829	88	2.5	521	2	S54266	glycoprotein GC -
757	89	2.5	1106	2	A97647	cation efflux syst	830	88	2.5	525	2	A35596	nuclear pore glyco
758	89	2.5	1106	2	AG2870	Acr family transpo	831	88	2.5	543	2	T33898	hypothetical prote
759	89	2.5	1145	2	B75625	hypothetical prote	832	88	2.5	562	2	A82743	probable malate de

833	88	2.5	564	1	HMIVC2	hemagglutinin prec	906	87.5	2.5	1735	1	S22812	DNA-directed RNA p
834	88	2.5	572	2	T12496	hypothetical prote	907	87.5	2.5	1752	1	S26849	DNA-directed RNA p
835	88	2.5	617	2	H75540	pyruvate dehydroge	908	87.5	2.5	1952	2	T48814	hypothetical prote
836	88	2.5	620	2	B81118	chaperone protein	909	87.5	2.5	6713	2	B89921	hypothetical prote
837	88	2.5	633	1	DNHUPA	polyadenylate-bind	910	87	2.5	288	2	S44256	fructosekinase (EC 2
838	88	2.5	637	2	AH3510	hypothetical membr	911	87	2.5	330	2	H95166	transcription regu
839	88	2.5	655	2	CT1438	hypothetical prote	912	87	2.5	330	2	G98032	hypothetical prote
840	88	2.5	658	2	DB1842	probable membrane	913	87	2.5	344	2	T31913	hypothetical prote
841	88	2.5	685	2	S67146	probable aldehyde	914	87	2.5	427	2	AC0203	chemotaxis MotB pr
842	88	2.5	741	2	D95966	probable membrane	915	87	2.5	458	2	B87335	hypothetical prote
843	88	2.5	805	2	T47241	RMW3/PIPI helicase	916	87	2.5	463	2	T14984	hypothetical prote
844	88	2.5	822	2	T25866	hypothetical prote	917	87	2.5	470	2	A30136	developmental cont
845	88	2.5	866	2	E69681	phosphoenolpyruvat	918	87	2.5	473	2	G97551	hypothetical prote
846	88	2.5	906	2	S03313	hypothetical prote	919	87	2.5	489	2	S62474	probable transcrip
847	88	2.5	933	2	A31930	cytoactin - chick	920	87	2.5	540	2	JC4916	signal transducing
848	88	2.5	982	2	T19526	hemolysin A toxin	921	87	2.5	560	2	AB0752	flagellar basal-bo
849	88	2.5	998	2	T00227	hypolysin A toxin	922	87	2.5	603	2	H82902	heat shock protein
850	88	2.5	1078	2	T42712	myelin transcripti	923	87	2.5	633	2	AE3258	cobT protein (limp
851	88	2.5	1080	2	T43164	lacta protein - Li	924	87	2.5	647	2	A45244	exo-alpha-sialidas
852	88	2.5	1115	1	IUMSNL	neural cell adhesi	925	87	2.5	651	2	A72384	conserved hypothet
853	88	2.5	1149	2	B84523	probable retroelem	926	87	2.5	658	2	DB1099	membrane-bound lyl
854	88	2.5	1213	2	T51032	hypothetical prote	927	87	2.5	720	1	A55160	Ttg protein - fru1
855	88	2.5	1273	2	S58782	SEC31 protein - ye	928	87	2.5	739	2	T21769	hypothetical prote
856	88	2.5	1308	2	T15280	hypothetical prote	929	87	2.5	764	2	F83161	hypothetical prote
857	88	2.5	1383	2	T13052	guanine nucleotide	930	87	2.5	770	1	A44337	pyocin protein PA3
858	88	2.5	1427	2	S22695	restin - human	931	87	2.5	782	2	E88556	kinesin-related pr
859	88	2.5	1469	2	T09219	basal transcrip tio	932	87	2.5	791	2	T41573	protein B0464.5c f
860	88	2.5	1472	2	A84470	hypothetical prote	933	87	2.5	796	2	A90541	hypothetical prote
861	88	2.5	1482	2	T34010	hypothetical prote	934	87	2.5	805	2	T40739	hypothetical prote
862	88	2.5	1562	2	T29146	hypothetical prote	935	87	2.5	837	2	S30971	rmx3-pilf helicase
863	88	2.5	1660	2	E85822	hypothetical prote	936	87	2.5	855	2	T32374	gene 26 protein -
864	88	2.5	2774	2	A43359	microbule-invasin Z	937	87	2.5	895	2	A43802	hypothetical prote
865	88	2.5	3434	1	GNMVMV	genome polypotein	938	87	2.5	980	2	G75523	probable cell divi
866	88	2.5	3591	1	S21010	filamentous hemag	939	87	2.5	1032	2	DB3637	serine/threonine p
867	88	2.5	3972	2	S75251	hypothetical prote	940	87	2.5	1137	2	A25018	circedian rhythm p
868	88	2.5	5376	2	T42215	zonadhesin - mouse	941	87	2.5	1173	2	T30308	rexa protein - Lac
869	87.5	2.5	223	2	T08672	hypothetical prote	942	87	2.5	1218	2	A26588	period clock prote
870	87.5	2.5	240	2	T33112	hypothetical prote	943	87	2.5	1248	2	C89874	autoalysin f (impro
871	87.5	2.5	335	2	DB3582	hypothetical prote	944	87	2.5	1262	2	T25168	hypothetical prote
872	87.5	2.5	342	2	S57652	transcription fact	945	87	2.5	1285	2	T14171	ataxin-2 - mouse
873	87.5	2.5	384	2	A44146	syndecan-3 - chick	946	87	2.5	1520	2	B82274	conserved hypothet
874	87.5	2.5	396	2	T02483	probable protein P	947	87	2.5	1589	2	TI3606	hypothetical prote
875	87.5	2.5	455	2	A87913	protein B0205.10 f	948	87	2.5	1609	2	S25345	probable membrane
876	87.5	2.5	467	2	F65020	echanolamine utill	949	87	2.5	1668	2	A60272	IgA-specific metal
877	87.5	2.5	469	2	T36496	probable dihydroli	950	87	2.5	1787	2	AG1360	probable tape-meas
878	87.5	2.5	474	2	T10011	probable penicilli	951	87	2.5	1839	1	RRPBM	genome polypotein
879	87.5	2.5	503	2	AH3535	periplasmic dipept	952	87	2.5	1955	1	AGCH	agrin precursor -
880	87.5	2.5	516	2	S37868	hypothetical prote	953	87	2.5	1957	2	T38077	hypothetical colle
881	87.5	2.5	546	2	T370735	a-type inclusion b	954	87	2.5	2453	2	S60254	nuclear receptor c
882	87.5	2.5	556	2	S51892	probable membrane	955	87	2.5	2890	2	F64669	DNA-directed RNA p
883	87.5	2.5	583	2	E75529	probable peptide A	956	87	2.5	2897	2	B48666	cell proliferation
884	87.5	2.5	594	2	B64018	hypothetical prote	957	87	2.5	3119	2	I49729	HD protein - mouse
885	87.5	2.5	597	2	AH2351	serine/threonine k	958	87	2.5	3256	2	A48666	cell proliferation
886	87.5	2.5	615	1	XXHU	dihydrolipoamide S	959	87	2.5	3716	2	E70969	probable pfb prote
887	87.5	2.5	648	2	FC4395	mucln 3 - human (f	960	87	2.5	4307	2	T20721	hypothetical prote
888	87.5	2.5	669	2	B42291	tail fiber protein	961	87.5	2.5	186	2	B70595	hypothetical prote
889	87.5	2.5	673	2	S35335	transcription fact	962	87.5	2.5	200	2	T30223	histone H1A - Afri
890	87.5	2.5	825	2	JS0174	cellulase (EC 3.2.	963	86.5	2.5	229	2	F72067	histone H1A - Afri
891	87.5	2.5	866	2	T45462	membrane glycoprot	964	86.5	2.5	257	2	F72067	diaminopimelate ep
892	87.5	2.5	871	1	XPBE12	major antigenic st	965	86.5	2.5	257	2	C86555	diaminopimelate ep
893	87.5	2.5	915	2	S36327	clathrin assembly	966	86.5	2.5	332	2	T32863	hypothetical prote
894	87.5	2.5	942	2	T37539	probable guanine n	967	86.5	2.5	358	1	A48952	triacylglycerol 11
895	87.5	2.5	971	2	B90835	probable tail fibre	968	86.5	2.5	367	2	S31651	MHC class I histoc
896	87.5	2.5	973	2	C85693	probable membrane	969	86.5	2.5	373	2	T51916	hypothetical prote
897	87.5	2.5	1029	2	T30351	mucln-like protein	970	86.5	2.5	395	2	H75457	hypothetical prote
898	87.5	2.5	1077	2	A44067	serine-rich protei	971	86.5	2.5	436	2	AH2171	homoserine dehydro
899	87.5	2.5	1099	2	B87608	cardiomyo-phosphat	972	86.5	2.5	437	2	A86911	probable serine/th
900	87.5	2.5	1120	2	H88449	protein F54D8.1 li	973	86.5	2.5	440	2	AC0962	D-serine dehydrata
901	87.5	2.5	1213	2	A41724	limb deformity (ld	974	86.5	2.5	467	2	JC7923	microtubule-associ
902	87.5	2.5	1240	2	JC5209	insulin receptor s	975	86.5	2.5	510	2	B69946	phage-related prot
903	87.5	2.5	1501	2	T58148	protein-tyrosine-p	976	86.5	2.5	515	2	A25048	regulatory protein
904	87.5	2.5	1530	2	AF1291	glutamate synthase	977	86.5	2.5	526	2	T33047	hypothetical prote
905	87.5	2.5	1711	2	T31337	1,4-beta-glucanase	978	86.5	2.5	546	2	AB0088	probable flagellar

979	86.5	2.5	547	2	T41213	probable zinc fing
980	86.5	2.5	578	2	F86484	transcription init
981	86.5	2.5	594	2	S62141	hypothetical prote
982	86.5	2.5	648	2	T09036	serine/threonine-s
983	86.5	2.5	658	2	T39500	homeotic protein s
984	86.5	2.5	667	2	S74254	hypothetical prote
985	86.5	2.5	685	2	T18964	Pept protein - Pse
986	86.5	2.5	687	2	T09051	gamma adducin - hu
987	86.5	2.5	701	2	JC7164	neurigin-3 [impo
988	86.5	2.5	713	2	T44447	type 4 fibrial bi
989	86.5	2.5	714	2	A83016	hypothetical prote
990	86.5	2.5	723	2	T38780	FOSION ribonuclea
991	86.5	2.5	730	2	A96988	HF-1 regulatory el
992	86.5	2.5	780	2	A48143	hypothetical prote
993	86.5	2.5	784	2	T20074	penicillin amidase
994	86.5	2.5	846	1	PNECA	hypothetical prote
995	86.5	2.5	850	2	T01847	protein F32D8.4 [1
996	86.5	2.5	870	2	A89201	cellulose synthase
997	86.5	2.5	881	2	B98320	pol polyprotein -
998	86.5	2.5	886	1	GNLJSP	endopeptidase Clp
999	86.5	2.5	908	1	S61476	phosphoprotein - f
1000	86.5	2.5	927	2	T38127	hypothetical prote
1001	86.5	2.5	1038	2	H90053	hypothetical prote
1002	86.5	2.5	1093	2	B86748	hypothetical prote
1003	86.5	2.5	1134	2	S53955	vesicle associated
1004	86.5	2.5	1180	2	E86719	proteinase related
1005	86.5	2.5	1249	2	T14150	rig-1 protein - mo
1006	86.5	2.5	1269	2	A90222	transcription-repa
1007	86.5	2.5	1344	2	T14316	probable multifunc
1008	86.5	2.5	1379	2	A81102	pyrimidine synthec
1009	86.5	2.5	1462	1	A69809	mucin 2, intestina
1010	86.5	2.5	1481	1	Q2DOP3	floculation prote
1011	86.5	2.5	1513	2	A54895	surface antigen pa
1012	86.5	2.5	1537	2	S53465	tensin - chicken
1013	86.5	2.5	1565	2	S04729	probable S-layer p
1014	86.5	2.5	1733	2	S27939	b1me protein - Eme
1015	86.5	2.5	1939	2	D97316	hypothetical prote
1016	86.5	2.5	2073	1	BMASBE	hypothetical prote
1017	86.5	2.5	2756	2	T30183	groovin gene prote
1018	86.5	2.5	4151	2	T13734	hypothetical prote
1019	86	2.5	126	2	T21762	arabinogalactan-11
1020	86	2.5	168	2	S52994	hypothetical prote
1021	86	2.5	226	2	T29210	hypothetical prote
1022	86	2.5	289	2	E81259	hypothetical prote
1023	86	2.5	344	2	T48827	hypothetical prote
1024	86	2.5	350	1	C70009	ABC transporter (1
1025	86	2.5	384	2	T32756	hypothetical prote
1026	86	2.5	413	2	S28066	sexual differentiation
1027	86	2.5	420	2	UC4716	zinc finger DNA-bl
1028	86	2.5	424	2	T33663	hypothetical prote
1029	86	2.5	442	2	G85878	D-serine dehydrata
1030	86	2.5	442	2	E91034	D-serine dehydrata
1031	86	2.5	461	2	S45568	nuclear factor I-A
1032	86	2.5	462	2	AH1184	wall associated pr
1033	86	2.5	494	2	H75587	conserved hypochet
1034	86	2.5	508	2	E70764	probable cobi prot
1035	86	2.5	509	2	JC5428	nuclear factor I f
1036	86	2.5	532	2	B36586	hook-containing pr
1037	86	2.5	538	2	S57459	acetylactate synth
1038	86	2.5	563	2	C97348	hemagglutinin prec
1039	86	2.5	567	1	HMIIV	ORF MSV069 probab
1040	86	2.5	575	2	T28230	probable hormone r
1041	86	2.5	601	1	ORMSN1	hypothetical prote
1042	86	2.5	638	2	T38863	hypothetical prote
1043	86	2.5	647	2	A84265	hypothetical prote
1044	86	2.5	658	2	A33598	endoglucanase 3 (S
1045	86	2.5	672	2	T20310	hypothetical prote
1046	86	2.5	702	2	S48754	major surface prot
1047	86	2.5	734	2	S25820	dynamun-related pr
1048	86	2.5	744	2	T42588	DNA-packaging prot
1049	86	2.5	738	2	T44194	hypothetical prote
1050	86	2.5	740	2	AD0485	probable exported
1051	86	2.5	795	2	T36588	probable penicilli
1052	86	2.5	798	2	T34248	hypothetical prote
1053	86	2.5	802	1	B44390	protein-tyrosine-P
1054	86	2.5	810	2	C72785	problein aldende
1055	86	2.5	842	2	H86220	hypothetical prote
1056	86	2.5	926	2	T39864	chitin synthase 2
1057	86	2.5	932	2	T45894	hypothetical prote
1058	86	2.5	937	2	E87640	TonB-dependent rec
1059	86	2.5	954	2	B86174	protein Flp19.26
1060	86	2.5	1027	2	F87370	alpha-L-rhamnosida
1061	86	2.5	1161	2	D83076	type 4 fibrial bi
1062	86	2.5	1218	2	A26427	period clock prote
1063	86	2.5	1331	2	T04938	hypothetical prote
1064	86	2.5	1340	2	A39608	proteoglycan core
1065	86	2.5	1348	2	AH1115	cell surface prote
1066	86	2.5	1495	2	A85240	hypothetical prote
1067	86	2.5	1495	2	T10649	hypothetical prote
1068	86	2.5	1702	2	T14050	protein kinase (EC
1069	86	2.5	1829	2	T14280	RNI protein - mous
1070	86	2.5	1962	2	A32634	lactocepin (EC 3.4
1071	86	2.5	2094	2	S33124	lpr protein - huma
1072	86	2.5	2256	2	AD1018	large repetitive p
1073	86	2.5	2377	2	T42630	aggreacan - bovine
1074	86	2.5	2761	2	T29285	hypothetical prote
1075	86	2.5	3157	2	B70969	probable PPB prote
1076	86	2.5	3452	2	T42730	Basoon protein -
1077	86	2.5	5105	2	T30250	hypothetical prote
1078	86	2.5	6260	2	T30228	polyketide synthas
1079	85.5	2.4	287	2	AB3395	biotin-lacetyl-CoA
1080	85.5	2.4	288	2	T21790	hypothetical prote
1081	85.5	2.4	319	2	B86433	hypothetical prote
1082	85.5	2.4	350	2	S61581	hypothetical prote
1083	85.5	2.4	364	2	T148188	gene NKX6.1 protel
1084	85.5	2.4	377	2	A48018	mucin 7 precursor,
1085	85.5	2.4	394	2	G84265	hypothetical prote
1086	85.5	2.4	430	2	S50604	AST2 protein - yea
1087	85.5	2.4	437	2	H64251	replicatoin initia
1088	85.5	2.4	451	2	A88641	protein F52C12.1 [
1089	85.5	2.4	467	2	E91043	ethanolamine utilil
1090	85.5	2.4	467	2	H85887	hypothetical prote
1091	85.5	2.4	522	2	S09996	nuclear factor I-A
1092	85.5	2.4	548	2	T32907	hypothetical prote
1093	85.5	2.4	561	2	A31256	transcription fac
1094	85.5	2.4	567	2	A62008	hypothetical prote
1095	85.5	2.4	576	2	A26628	homeotic protein I
1096	85.5	2.4	601	2	T31466	cell-division prot
1097	85.5	2.4	616	2	AF0263	proteinas IV (EC
1098	85.5	2.4	624	2	T33868	hypothetical prote
1099	85.5	2.4	659	2	C65922	yfgc protein - Ebc
1100	85.5	2.4	671	2	AC1183	transketolase homo
1101	85.5	2.4	695	2	D90468	copper-transportin
1102	85.5	2.4	698	2	T17261	hypothetical prote
1103	85.5	2.4	718	2	G97249	transcription acce
1104	85.5	2.4	730	2	T16455	hypothetical prote
1105	85.5	2.4	734	2	T52535	suppressor of A-ki
1106	85.5	2.4	747	2	B85499	outer membrane rec
1107	85.5	2.4	747	2	B90648	outer membrane rec
1108	85.5	2.4	758	2	A29253	finger protein hun
1109	85.5	2.4	806	2	B69637	DNA gyrase-like pr
1110	85.5	2.4	825	2	T29634	hypothetical prote
1111	85.5	2.4	832	2	AD1096	internatin protein
1112	85.5	2.4	886	1	UC5085	replication licens
1113	85.5	2.4	904	2	AH2019	hypothetical prote
1114	85.5	2.4	922	2	F81539	polymorphic membra
1115	85.5	2.4	922	2	B72131	polymorphic outer
1116	85.5	2.4	922	2	B86491	polymorphic outer
1117	85.5	2.4	927	2	AH1369	transmembrane prot
1118	85.5	2.4	930	2	T20817	hypothetical prote
1119	85.5	2.4	1001	2	T13807	potasssium channel
1120	85.5	2.4	1037	2	T05309	probable glycine d
1121	85.5	2.4	1054	2	T43226	translacion initia
1122	85.5	2.4	1131	2	T15787	hypothetical prote
1123	85.5	2.4	1133	2	T22976	hypothetical prote
1124	85.5	2.4	1139	2	B54962	sterol regulatory

1125	85.5	2.4	1142	2	S36845	1198	85	2.4	1289	2	T18212	paraaporal crystal
1126	85.5	2.4	1147	2	T40866	1199	85	2.4	1334	2	T50568	probable multi-dom
1127	85.5	2.4	1182	2	S14916	1200	85	2.4	1495	2	S60255	transcription co-r
1128	85.5	2.4	1221	2	T23472	1201	85	2.4	1582	2	AC1153	adhesin homolog lm
1129	85.5	2.4	1241	2	T18311	1202	85	2.4	1633	2	T01879	hypothetical prote
1130	85.5	2.4	1281	2	JC5368	1203	85	2.4	1873	2	T30944	hypothetical prote
1131	85.5	2.4	1309	2	T13158	1204	85	2.4	2015	2	B81989	surface protein pr
1132	85.5	2.4	1436	2	UQ2294	1205	85	2.4	2470	2	T50726	cation-independent
1133	85.5	2.4	1458	2	A45665	1206	85	2.4	3328	2	T30835	breast cancer tumo
1134	85.5	2.4	1460	2	S48457	1207	85	2.4	3430	1	GNMWV	genome polypeptid
1135	85.5	2.4	1816	1	S68960	1208	85	2.4	3938	2	T42761	Bassoon protein -
1136	85.5	2.4	3329	2	T30904	1209	84.5	2.4	229	2	C97030	arginase (imported
1137	85.5	2.4	6658	2	T13931	1210	84.5	2.4	322	2	B84635	hypothetical prote
1138	85	2.4	128	2	T05635	1211	84.5	2.4	337	2	S42479	glyceroldehyde-3-p
1139	85	2.4	192	2	S53591	1212	84.5	2.4	384	2	A70805	probable lpxn prot
1140	85	2.4	209	2	B87589	1213	84.5	2.4	396	2	T10951	naringenin-chalcon
1141	85	2.4	238	2	T26419	1214	84.5	2.4	412	2	C72548	probable dihydroli
1142	85	2.4	319	2	B35090	1215	84.5	2.4	413	2	A55238	transcription fact
1143	85	2.4	339	2	G70915	1216	84.5	2.4	444	2	F86329	hypothetical prote
1144	85	2.4	376	2	S36247	1217	84.5	2.4	445	2	AH2480	hypothetical prote
1145	85	2.4	387	2	AC3618	1218	84.5	2.4	532	2	T49467	related to GOp1-in
1146	85	2.4	397	2	A99907	1219	84.5	2.4	536	2	T17217	hypothetical prote
1147	85	2.4	408	2	B87436	1220	84.5	2.4	543	2	A41211	early growth respo
1148	85	2.4	413	2	T26040	1221	84.5	2.4	570	2	D97738	hypothetical prote
1149	85	2.4	418	2	T16713	1222	84.5	2.4	572	2	B46529	Ig Y heavy chain (
1150	85	2.4	442	2	DMECS	1223	84.5	2.4	572	2	S73901	ABC transporter y)
1151	85	2.4	469	2	A83411	1224	84.5	2.4	600	2	E86854	hypothetical prote
1152	85	2.4	474	2	S15921	1225	84.5	2.4	609	1	A42358	vibriolysin (EC 3
1153	85	2.4	482	2	AG1147	1226	84.5	2.4	609	2	G87496	peptidase, M23/M3
1154	85	2.4	484	2	A41487	1227	84.5	2.4	636	2	T38473	probable serine/th
1155	85	2.4	511	1	UQ1935	1228	84.5	2.4	636	2	S63131	probable membrane
1156	85	2.4	511	1	IQMLC	1229	84.5	2.4	658	2	S60170	protein kinase Pak
1157	85	2.4	535	2	S65762	1230	84.5	2.4	662	2	T41442	omnipotent nonsens
1158	85	2.4	539	2	S40900	1231	84.5	2.4	666	2	H75295	transketolase - De
1159	85	2.4	540	2	JC4917	1232	84.5	2.4	697	2	T03834	nuclear distributi
1160	85	2.4	550	1	A40449	1233	84.5	2.4	706	2	D84466	hypothetical prote
1161	85	2.4	572	1	VGNZBA	1234	84.5	2.4	719	2	T52510	hypothetical prote
1162	85	2.4	600	2	S07638	1235	84.5	2.4	729	2	E70803	hypothetical prote
1163	85	2.4	626	1	NBHUIA	1236	84.5	2.4	737	2	H95882	probable aldehyde
1164	85	2.4	626	2	S53871	1237	84.5	2.4	747	1	ORCFE	ferrichrome-iron r
1165	85	2.4	646	2	S56201	1238	84.5	2.4	755	2	T20950	hypothetical prote
1166	85	2.4	673	2	S11840	1239	84.5	2.4	758	2	A10609	ATP-dependent Clp
1167	85	2.4	689	2	A83036	1240	84.5	2.4	758	2	AB0167	ATP-dependent Clp
1168	85	2.4	693	2	C70167	1241	84.5	2.4	758	2	T31994	hypothetical prote
1169	85	2.4	693	2	T19551	1242	84.5	2.4	775	2	F98136	hypothetical prote
1170	85	2.4	715	2	S76492	1243	84.5	2.4	786	2	T16509	hypothetical prote
1171	85	2.4	725	2	F81845	1244	84.5	2.4	821	2	AD1507	probable secreted
1172	85	2.4	747	2	T34329	1245	84.5	2.4	835	2	T34770	probable protein p
1173	85	2.4	750	2	S06726	1246	84.5	2.4	903	2	D87250	DNA mismatch repai
1174	85	2.4	750	2	F95039	1247	84.5	2.4	928	2	G86546	polymorphic oute
1175	85	2.4	750	2	H97909	1248	84.5	2.4	928	2	G81591	polymorphic membra
1176	85	2.4	751	2	F69338	1249	84.5	2.4	941	2	S78633	isoleucine-tRNA li
1177	85	2.4	781	2	S37032	1250	84.5	2.4	967	1	SYMFA	alanine-tRNA ligas
1178	85	2.4	789	2	S44759	1251	84.5	2.4	968	2	T41078	hemolysin - Escher
1179	85	2.4	841	2	S69563	1252	84.5	2.4	1018	2	AG0703	conserved hypochet
1180	85	2.4	859	2	B90768	1253	84.5	2.4	1021	2	T15765	hypothetical prote
1181	85	2.4	907	2	A45560	1254	84.5	2.4	1035	2	A64686	cation efflux syst
1182	85	2.4	936	2	D97630	1255	84.5	2.4	1065	2	D97225	carbamoylphosphate
1183	85	2.4	946	1	IYHU2	1256	84.5	2.4	1117	2	S63399	probable membrane
1184	85	2.4	958	2	S45466	1257	84.5	2.4	1117	2	A39962	kinase-related tra
1185	85	2.4	970	2	E70533	1258	84.5	2.4	1133	2	T15617	hypothetical prote
1186	85	2.4	982	2	T34830	1259	84.5	2.4	1148	2	AD0198	transcription-repa
1187	85	2.4	1015	2	JC6552	1260	84.5	2.4	1148	2	F86403	probable transposo
1188	85	2.4	1059	2	B87058	1261	84.5	2.4	1150	2	S58775	mypl protein - smu
1189	85	2.4	1091	2	A44147	1262	84.5	2.4	1181	2	C86349	F8K7.4 protein - A
1190	85	2.4	1120	2	T01863	1263	84.5	2.4	1187	2	T31351	endo-1,4-beta-xyla
1191	85	2.4	1140	2	B70729	1264	84.5	2.4	1215	2	S50428	probable Ca2+-tran
1192	85	2.4	1203	2	T01287	1265	84.5	2.4	1216	2	T34101	hypothetical prote
1193	85	2.4	1217	2	T25894	1266	84.5	2.4	1223	2	T15316	hypothetical prote
1194	85	2.4	1246	2	AC2372	1267	84.5	2.4	1235	2	T16346	hypothetical prote
1195	85	2.4	1270	2	T30339	1268	84.5	2.4	1442	2	T42607	transcription acti
1196	85	2.4	1273	1	TDRTT	1269	84.5	2.4	1468	2	A44345	nucleoporin - rat
1197	85	2.4	1274	2	E81779	1270	84.5	2.4	1520	1	TVFPA	protein-tyrosine k

1271	84.5	2.4	1560	2	T02885	peroxisome prolif	1344	84	2.4	1280	2	T00365	hypothetical prote
1272	84.5	2.4	1791	2	T02345	hypothetical prote	1345	84	2.4	1289	2	E90098	RNA polymerase III
1273	84.5	2.4	1819	2	D97033	uncharacterized pr	1346	84	2.4	1299	2	E30341	zinc finger protei
1274	84.5	2.4	2059	2	D82671	surface protein XP	1347	84	2.4	1401	2	T48079	hypothetical prote
1275	84.5	2.4	2130	2	AB0821	probable exported	1348	84	2.4	1430	2	T12449	hypothetical prote
1276	84.5	2.4	3149	1	Q0888	BLU1 protein - hu	1349	84	2.4	1518	2	S37928	probable purine nu
1277	84.5	2.4	3344	2	U01899	genome polypotein	1350	84	2.4	1570	2	AC2012	hypothetical prote
1278	84	2.4	259	2	E69276	conserved hypochet	1351	84	2.4	1601	2	AB1730	hypothetical prote
1279	84	2.4	280	2	AB4117	flagellar hook-bas	1352	84	2.4	1655	2	T32633	hypothetical prote
1280	84	2.4	317	2	S55316	nucin (clone PGM-2	1353	84	2.4	1829	2	T24583	hypothetical prote
1281	84	2.4	336	2	T15837	hypothetical prote	1354	84	2.4	2043	2	T18524	scavenger receptor
1282	84	2.4	341	2	T48858	acetylpolymaine am	1355	84	2.4	2061	2	T13751	transcription fact
1283	84	2.4	346	2	A99173	hypothetical prote	1356	84	2.4	2430	1	A34971	protein-tyrosine-p
1284	84	2.4	347	2	H95406	conserved hypochet	1357	84	2.4	2523	2	F70846	probable ppe prote
1285	84	2.4	346	2	S10571	mucin 1 precursor,	1358	84	2.4	2630	2	T08868	polyprotein PI - A
1286	84	2.4	402	2	E86185	hypothetical prote	1359	84	2.4	3295	2	AE0074	probable adhesin Y
1287	84	2.4	416	2	A55237	transcription fact	1360	83.5	2.4	212	2	S71114	ribosomal protein
1288	84	2.4	437	2	S15306	CMP-4-keto-6-deoxy	1361	83.5	2.4	299	1	G69263	MU1232 protein hom
1289	84	2.4	440	2	E71293	hypothetical prote	1362	83.5	2.4	302	2	A84062	ferrichrome ABC tr
1290	84	2.4	441	2	T31482	hypothetical prote	1363	83.5	2.4	335	2	S08341	myristylated alani
1291	84	2.4	448	2	A27631	cellulase (EC 3.2.	1364	83.5	2.4	341	1	DEJWG	glyceraldhyde-3-P
1292	84	2.4	473	1	A53036	Ca2+/calmodulin-de	1365	83.5	2.4	345	2	E88103	protein M10G11.5 l
1293	84	2.4	491	2	H84477	probable pita-like	1366	83.5	2.4	361	2	E84678	probable carboxype
1294	84	2.4	491	2	F70659	probable pbpa prot	1367	83.5	2.4	398	2	A35281	integumentary muc
1295	84	2.4	496	2	S00855	hypothetical prote	1368	83.5	2.4	409	2	A43446	RAD3 protein homo
1296	84	2.4	502	2	T24227	hypothetical prote	1369	83.5	2.4	418	2	E90841	probable trehalase
1297	84	2.4	529	2	H84049	hypothetical prote	1370	83.5	2.4	428	2	EC5338	3-phosphosialkimate
1298	84	2.4	546	2	AG0586	phosphoglucomutase	1371	83.5	2.4	447	2	F82862	conjugal transfer
1299	84	2.4	549	2	A90253	hypothetical prote	1372	83.5	2.4	449	2	B86763	hypothetical prote
1300	84	2.4	563	2	T04359	pectin methylster	1373	83.5	2.4	450	2	C90608	hypothetical prote
1301	84	2.4	572	2	AC1200	phosphotransferase	1374	83.5	2.4	463	2	E70657	hypothetical prote
1302	84	2.4	572	2	A11557	phosphotransferase	1375	83.5	2.4	468	2	A70065	hypothetical prote
1303	84	2.4	584	2	T19061	hypothetical prote	1376	83.5	2.4	482	2	D85913	succinate-semialde
1304	84	2.4	597	2	T35746	hypothetical prote	1377	83.5	2.4	482	2	B91069	trehalase, peripla
1305	84	2.4	607	2	T25922	hypothetical prote	1378	83.5	2.4	485	2	D85699	2-isopropylmalate
1306	84	2.4	633	2	AH1598	acylttransferase (c	1379	83.5	2.4	489	2	E63959	nucleoid DNA-bind
1307	84	2.4	639	2	S70126	hypothetical prote	1380	83.5	2.4	502	2	T01896	glycoprotein C - h
1308	84	2.4	659	1	B44212	structural protein	1381	83.5	2.4	511	1	VGBEF4	glycoprotein C - h
1309	84	2.4	676	2	AB2417	hypothetical prote	1382	83.5	2.4	511	1	VGBEF4	glycoprotein C - h
1310	84	2.4	677	2	E70722	hypothetical prote	1383	83.5	2.4	518	2	T49778	hypothetical prote
1311	84	2.4	679	2	T52163	hypothetical prote	1384	83.5	2.4	519	1	JX0166	NADH oxidase (hydr
1312	84	2.4	695	2	E86637	cell division prot	1385	83.5	2.4	545	2	D87259	phosphoglucomutase
1313	84	2.4	695	2	S28533	tna protein - lact	1386	83.5	2.4	556	2	UC5132	alpha-amylase (EC
1314	84	2.4	702	2	G01840	T-box protein 2 -	1387	83.5	2.4	565	2	S04782	alpha, alpha-trehal
1315	84	2.4	710	1	Q08E22	membrane antigen g	1388	83.5	2.4	582	2	T07952	lectin-like protei
1316	84	2.4	712	2	G91280	aerobic ribonuci	1389	83.5	2.4	601	2	T37738	hypothetical prote
1317	84	2.4	712	2	G86121	anaerobic ribonuci	1390	83.5	2.4	601	2	JC4576	serine proteinase
1318	84	2.4	727	2	A88131	protein F10G7.9 [i	1391	83.5	2.4	616	2	C75588	conserved hypochet
1319	84	2.4	732	2	S47688	cd2+-exporting ATP	1392	83.5	2.4	617	2	T16189	hypothetical prote
1320	84	2.4	814	2	A71419	probable allene ox	1393	83.5	2.4	630	2	A81903	probable chaperone
1321	84	2.4	820	2	B72575	hypothetical prote	1394	83.5	2.4	633	2	S62057	proline-rich prote
1322	84	2.4	823	2	C81835	probable P-type ca	1395	83.5	2.4	638	1	C69126	ferrous iron trans
1323	84	2.4	823	2	D81129	cation transport A	1396	83.5	2.4	638	1	XXAV	dihydroliopamide S
1324	84	2.4	827	2	F72414	ribonucleotide red	1397	83.5	2.4	644	2	D85359	hypothetical prote
1325	84	2.4	832	2	AB1452	hypothetical prote	1398	83.5	2.4	647	2	T41121	heat shock protein
1326	84	2.4	834	2	T42702	hypothetical prote	1399	83.5	2.4	668	2	T26724	hypothetical prote
1327	84	2.4	851	2	S67285	NMD1 protein - yea	1400	83.5	2.4	682	2	A42121	transcription fact
1328	84	2.4	865	2	T41685	probable gamma-aa	1401	83.5	2.4	694	2	S68442	Grb2-associated bi
1329	84	2.4	866	2	D44234	fibrinogen alpha c	1402	83.5	2.4	712	1	S69782	outer membrane pro
1330	84	2.4	876	2	T49801	hypothetical prote	1403	83.5	2.4	714	2	D87179	probable fatty oxi
1331	84	2.4	878	2	AH2075	ferrichrome-iron r	1404	83.5	2.4	728	2	T26607	hypothetical prote
1332	84	2.4	897	1	A39255	cytokine receptor	1405	83.5	2.4	752	1	C2HU	complement C2 prec
1333	84	2.4	935	2	E84491	hypothetical prote	1406	83.5	2.4	756	2	E82236	ATP-dependent Clp
1334	84	2.4	940	2	D89723	protein F39D8.1b l	1407	83.5	2.4	759	2	D84301	cell division cycl
1335	84	2.4	945	2	T21998	hypothetical prote	1408	83.5	2.4	762	2	H87466	beta-D-glucosidase
1336	84	2.4	1026	2	AE0771	probable RND-famil	1409	83.5	2.4	793	2	S34830	kinasin-related pr
1337	84	2.4	1041	2	S55862	probable membrane	1410	83.5	2.4	809	2	T41645	probable spindie p
1338	84	2.4	1042	2	T29307	hypothetical prote	1411	83.5	2.4	824	2	T23096	hypothetical prote
1339	84	2.4	1070	2	C75506	hypothetical prote	1412	83.5	2.4	851	2	D87252	TonB-dependent rec
1340	84	2.4	1171	2	T42372	probable guanilate	1413	83.5	2.4	852	2	C98310	haas protein (Y089
1341	84	2.4	1192	2	T08609	hypothetical prote	1414	83.5	2.4	870	2	T30110	hypothetical prote
1342	84	2.4	1219	2	S54570	probable membrane	1415	83.5	2.4	896	2	AB2825	aconitate hydratase
1343	84	2.4	1271	2	D64237	hypothetical prote	1416	83.5	2.4	898	2	T26577	hypothetical prote

1417	83.5	2.4	923	2	AH2972	heme receptor hasr
1418	83.5	2.4	988	1	QOBE24	nuclear antigen EB
1419	83.5	2.4	989	2	T47503	hypothetical prote
1420	83.5	2.4	989	2	T01519	hypothetical prote
1421	83.5	2.4	1003	2	C71139	hypothetical prote
1422	83.5	2.4	1013	2	G71460	probable outer mem
1423	83.5	2.4	1014	2	T13476	hypothetical prote
1424	83.5	2.4	1016	2	S30236	genome polypotein
1425	83.5	2.4	1062	2	B26330	hypothetical prote
1426	83.5	2.4	1063	2	T03743	bifocal protein -
1427	83.5	2.4	1065	2	S19482	hypothetical prote
1428	83.5	2.4	1179	2	T04488	DNA topoisomerase
1429	83.5	2.4	1215	2	T00364	hypothetical prote
1430	83.5	2.4	1230	2	T07663	soluble starch syn
1431	83.5	2.4	1232	2	B39432	ATP-dependent deox
1432	83.5	2.4	1244	2	T19068	hypothetical prote
1433	83.5	2.4	1255	2	T31065	diaphanous protein
1434	83.5	2.4	1292	2	T31462	probable magnesium
1435	83.5	2.4	1312	2	B35006	beta-N-acetylhexos
1436	83.5	2.4	1320	2	JC5630	TCOP1 protein - mo
1437	83.5	2.4	1329	2	C69048	cobalamin biosynth
1438	83.5	2.4	1607	1	MMMS2	laminin gamma-1 ch
1439	83.5	2.4	1694	2	H64106	IgA-specific metal
1440	83.5	2.4	1702	2	A41859	IgA-specific metal
1441	83.5	2.4	1706	2	B44939	zinc finger protei
1442	83.5	2.4	1732	2	T30836	lysine-specific cy
1443	83.5	2.4	1824	1	QRHUMT	microtubule-associ
1444	83.5	2.4	2450	2	S71625	protein-tyrosine-p
1445	83.5	2.4	2471	2	T03820	probable histidine
1446	83.5	2.4	2845	2	T19505	adenomatous polyp
1447	83.5	2.4	3122	2	T17202	DNA-directed DNA p
1448	83.5	2.4	3329	2	T42205	breast cancer susc
1449	83.5	2.4	4545	1	S25111	alpha-2-macroglobu
1450	83	2.4	285	2	D69835	alcohol dehydrogen
1451	83	2.4	340	2	T09663	glyceraledehyde-3-p
1452	83	2.4	340	2	T28080	hypothetical prote
1453	83	2.4	351	1	RWHUC2	T-cell surface gly
1454	83	2.4	372	2	T21757	hypothetical prote
1455	83	2.4	376	2	T39138	hypothetical prote
1456	83	2.4	386	2	S45569	nuclear factor I-A
1457	83	2.4	390	1	QOBE77	glycoprotein I pre
1458	83	2.4	400	2	C75336	serine proteinase,
1459	83	2.4	414	2	AL2544	hypothetical prote
1460	83	2.4	440	2	T86698	hypothetical prote
1461	83	2.4	445	2	S00256	Krox-20 protein -
1462	83	2.4	450	2	S73419	signal recognition
1463	83	2.4	451	1	S68455	serine/threonine-s
1464	83	2.4	452	2	C97162	UDP-N-acetylmuram
1465	83	2.4	470	2	D84863	hypothetical prote
1466	83	2.4	482	2	T22981	hypothetical prote
1467	83	2.4	487	2	PQ0259	hypothetical prote
1468	83	2.4	495	2	C83598	hypothetical prote
1469	83	2.4	524	2	P86572	protein F12M16.10
1470	83	2.4	534	2	S75472	GTP-binding protei
1471	83	2.4	546	2	G90558	phosphoglucomutase
1472	83	2.4	546	2	G90578	phosphoglucomutase
1473	83	2.4	553	2	I37417	glycerol kinase -
1474	83	2.4	553	2	C75318	hypothetical prote
1475	83	2.4	561	2	B83754	arginine-tRNA liga
1476	83	2.4	567	2	T16625	asparagine synthas
1477	83	2.4	578	2	G82950	conserved hypotet
1478	83	2.4	587	2	A56015	finger protein SIG
1479	83	2.4	589	2	G69815	ABC transporter (A
1480	83	2.4	593	2	JC4175	acid phosphatase (
1481	83	2.4	603	2	A82753	dihydropyrimidin
1482	83	2.4	638	2	H82630	hypothetical prote
1483	83	2.4	650	2	AB2004	hypothetical prote
1484	83	2.4	677	2	T39713	zinc finger protei
1485	83	2.4	690	2	H86464	hypothetical prote
1486	83	2.4	703	2	T24975	hypothetical prote
1487	83	2.4	705	2	T30521	surface protein -
1488	83	2.4	706	2	B30411	synapsin Ia - Dovi
1489	83	2.4	707	2	A46691	E-box-binding prot

1490	83	2.4	708	1	M2XR1L	structural protein
1491	83	2.4	708	1	M2XR2J	structural protein
1492	83	2.4	712	1	A47331	ribonucleoside-tri
1493	83	2.4	722	2	T22359	hypothetical prote
1494	83	2.4	728	2	F72693	probable phospho
1495	83	2.4	729	2	T51896	probable translati
1496	83	2.4	738	2	T40035	hypothetical prote
1497	83	2.4	803	2	A86655	hypothetical prote
1498	83	2.4	843	2	A87275	tonB-dependent rec
1499	83	2.4	846	2	S52418	GMP-binding regula
1500	83	2.4	854	1	XYBT1	protein N-acetyltr

ALIGNMENTS

RESULT 1

A40020 collagen alpha 1(XII) chain precursor - chicken

N/Alternate names: fibrochimerin

C/Species: Gallus gallus (chicken)

C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C/Accession: A40020, A34485, B34485, A28037, S23814, S22554, S28811

R/Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Niehida, Y.; Obar

J. Cell Biol. 115, 209-221, 1991

A/Title: The complete primary structure of type XII collagen shows a chimeric molecule w

nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.

A/Reference number: A40020; MUID:92011862; PMID:1918137

A/Accession: A40020

A/Molecule type: mRNA

A/Residues: 1-3124 <YMS>

A/Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:9222810; PIDN:

A/Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,

R/Gordon, M.K.; Gerecke, D.R.; Dubler, B.; van der Rest, M.; Olsen, B.R.

J. Biol. Chem. 264, 19772-19778, 1989

A/Title: Type XII collagen. A large multidomain molecule with partial homology to type I.

A/Reference number: A34485; MUID:9062079; PMID:2584192

A/Accession: A34485

A/Molecule type: mRNA

A/Residues: 2456-2758 'A', 2760-2802 'F', 2804-2976 'F', 2978-3124 <GOR>

A/Cross-references: UNIPARC:UPI000011233; EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PI

A/Accession: B34485

A/Molecule type: protein

A/Residues: 2772-2792;2846-2873 <GOR2>

A/Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40

A/Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c

A/Reference number: A28037; MUID:87317590; PMID:3476925

A/Accession: A28037

A/Molecule type: mRNA

A/Residues: 2960-2976 'F', 2978-3074 'AG', <GOR3>

A/Cross-references: UNIPARC:UPI000011274; EMBL:M17375; NID:9211649; PIDN:AAA48718.1; PI

A/Note: this sequence has been revised in reference A34485

R/Koch, M.; Bernasconi, C.; Chiquet, M.

Eur. J. Biochem. 207, 847-856, 1992

A/Title: A major oligomeric fibroblast procollagen identified as a novel large form of

A/Reference number: S23814; MUID:92362621; PMID:1323460

A/Accession: S23814

A/Molecule type: protein

A/Residues: 'X', '133', 'Q', '1335-1347;1914-1928;2504', 'X', '2506', 'X', '2508-2511', 'X', '2513-2517 <

A/Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43

R/Dublet, B.; van der Rest, M.

J. Biol. Chem. 262, 17724-17727, 1987

A/Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-

A/Reference number: S22254; MUID:88087065; PMID:3121603

A/Accession: S22254

A/Molecule type: protein

A/Residues: 2831-2832, 'T', 2834, 'R', 2836-2843;3002-3014 <DUB>

A/Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45

R/Trueb, U.; Trueb, B.

Biochim. Biophys. Acta 1171, 97-98, 1992

A/Title: The two splice variants of collagen XII share a common 5' end.

[illegible]

Db 416 TIMEKTQGVK-----:QVECSRGVDVAKADVVELFDVGSSYSIGIANPVKRAFLFELVKS 468

Qy 525 FEISDTDRICAVQTYTEBRLFEFPDKSSKPDILNAIKRGVWGSGETSGAINFALQ 584

Db 469 FEISPRKVOISLVQVSRDPMHEFSLNRYNRVKDIIQAINTEFPYGGSTNGKAWTYREK 528

Qy 585 LF---KSKSPNKRKMLITLTDGRSYDDVIRIPMAALAKGVITAIQVAAAOEELEVIAT 641

Db 529 VFTVTSKSGRPNVPRWMLITLTDGSSSDAFKEPAIKLMDADVEIRAVGVKDAVTELEAIAS 588

Qy 642 HPARDHSFFVDEFDNLHQYVPRIIQNTCTEENSO 675

Db 589 PPAETHVYTVDEDFDAFORISFELTOSVCLRIEOD 622

RESULT 2

A37797

collagen alpha 3(VI) chain precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004

C:Accession: A37797; A34270; A32674

R:Doliana, R.; Bonaldo, P.; Colombatti, A.

J:Cell Biol. 111, 2197-2205, 1990

A:Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternative splicing

A:Reference number: A37797; PMID:1977751

A:Accession: A37797

A:Molecule type: mRNA

A:Residues: 1-253;112-321;434-453;504-518;635-655;704-717;832-853 <DOL>

A:Cross-references: UNIPROT: P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32; UNIPARC:UPI0000173C33; UNIPARC:UPI0000173C34; UNIPARC:UPI0000173C35

R:Bonaldo, P.; Russo, V.; Buccicotti, F.; Doliana, R.; Colombatti, A.

Biochemistry 29, 1245-1254, 1990

A:Title: Structural and functional features of the alpha3 chain indicate a bridging role

A:Reference number: A34270; PMID:90212613; PMID:2322559

A:Accession: A34270

A:Molecule type: mRNA

A:Residues: 224-2871 <BON>

A:Cross-references: UNIPARC:UPI0000173C38; GB:M24282

A:Note: The authors translated the codon TTC for residue 1916 as Leu and TTC for residue 1917 as Ile.

J: Biol. Chem. 264, 20235-20239, 1989

A:Title: The carboxyl termini of the chicken alpha3 chain of collagen VI is a unique motif

A:Reference number: A32674; PMID:90062147; PMID:2584214

A:Accession: A32674

A:Molecule type: mRNA

A:Residues: 2151-2199; 2792-3137 <BO2>

A:Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282

C:Genetics:

A:Introns: 30/1; 236/1; 437/1; 638/1; 838/1

C:Superfamily: collagen VI

C:Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracellular matrix

F:1-25/Domain: signal sequence #status predicted <SIG>

F:126-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>

F:126-2042/Domain: non-collagenous #status predicted <NNC>

F:136-202/Domain: von Willebrand factor type A repeat homology <VM01>

F:1239-404/Domain: von Willebrand factor type A repeat homology <VM02>

F:1442-607/Domain: von Willebrand factor type A repeat homology <VM03>

F:1642-807/Domain: von Willebrand factor type A repeat homology <VM04>

F:1840-1004/Domain: von Willebrand factor type A repeat homology <VM05>

F:1033-1197/Domain: von Willebrand factor type A repeat homology <VM06>

F:11237-1400/Domain: von Willebrand factor type A repeat homology <VM07>

F:11439-1604/Domain: von Willebrand factor type A repeat homology <VM08>

F:11639-1804/Domain: von Willebrand factor type A repeat homology <VM09>

F:11838-2010/Domain: von Willebrand factor type A repeat homology <VM10>

F:12043-2378/Domain: collagenous #status predicted <COL>

F:12045-2047/Region: cell attachment (R-G-D) motif

F:12153-2155/Region: cell attachment (R-G-D) motif

F:12159-2161/Region: cell attachment (R-G-D) motif

F:12379-2137/Domain: non-collagenous #status predicted <NC>

F:12405-2577/Domain: von Willebrand factor type A repeat homology <VM11>

F:12623-2806/Domain: von Willebrand factor type A repeat homology <VM12>

F:12803-2846/Domain: platelet glycoprotein Ib-like #status predicted <GPI>

F:2954-1039/Domain: fibronectin type III repeat homology <FN3>
 F:3072-3122/Domain: animal knitz-type proteinase inhibitor homology <BPI>
 F:201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (asn) (covalent

Query Match 14.4% Score 504.5; DB 2; Length 3137;
 Best Local Similarity 30.7%; Pred. No. 8,9e-25;
 Matches 121; Conservative 87; Mismatches 155; Indels 31; Gaps 8;

QY 293 DLSFLIDGSTSIGKRRFRIOKQLADVAQALDIGPAGLGVGVGYDGNPAPHILKTHN 352
 Db 38 DIFLVDSMSIGKEHFQVREFLVDYVKALDVGNDPRFALVQPSGNPHTEPOLNTYPS 97
 QY 353 SRDLTAIEKTIQGGLSNVGRAISFVTKNFFSKANGRS--GAPNVVVVAVDGPPTDKV 410
 Db 98 NQDVLSTANMPYWGSGSKTGLEYLLENHLYKAAGSRASEGVPQVYIVLTDDGOSODV 157
 QY 411 EEARLARESGINIFITIEGAENEKQYVVEPNPANKAVCTRTGFSLVHOSFGLHKT 470
 Db 158 ALPSSVLKSAHVMIAVGVQDAVEGELKEIASRPDT-----HIFNLENTALHGI 208
 QY 471 LQPLVK--RVCDTDLRLACSK-----TCINSGADIGFVIDGSSSVGTGNFTVLQFVNTLT 522
 Db 209 VGDVLASVRSMTGEQAGAKGLVDITQESADILFLIDGSDNIGSVAFQAIRFIVNLI 268
 QY 523 KEFEISTDTIRIGAVQTYEQRLEFGFDKYSKPDILNAIKRVGVWSG-GTSTGAALNEA 581
 Db 269 ESLRVGAQOIHIGVQVSDQPRTEFALNSYSTKADVLDAVKALSFPGCKEANTGALEYV 328
 QY 582 LEOLFKKSPKPK-----RKLMLITDGRSYDVRIPMAAHLKGVITYAIGVAAQEELE 636
 Db 329 VENLTQGGSRIEAVPQIIVLISGESSDDIREGLAVKQASIFSFISGLVNAISAEL 388
 QY 637 EVIATHPARDSFEVDEFD--NLHQVPRIIQNI 668
 Db 389 QQIAT----DGFATLDIRNLALRELLPNI 418

RESULT 3

A337979
 cartilage matrix protein precursor - human

C:Species: Homo sapiens (man)
 C:Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004

C:Accession: A37979; B37979
 R:Junkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Shi, J. Biol. Chem. 265, 19624-19631, 1990

A:Title: Structure and chromosomal location of the human gene encoding cartilage matrix A:Reference number: A37979; MUID:91060568; PMID:2246248

A:Accession: A37979
 A:Molecule type: DNA

A:Residues: 1-496 <JEN>
 A:Cross-references: UNIPROT:P21941; UNIPARC:UPI00004F1ED; GB:J05667

A:Accession: B37979
 A:Molecule type: mRNA

A:Residues: 157-290, 'L', 292-496 <JB2>
 A:Cross-references: UNIPARC:UPI000016A6B9; GB:M55683; GB:J05666; GB:J05667; NID:9180651;

C:Genetics:
 A:Gene: GDB:CRM

A:Cross-references: GDB:127280; OMIM:115437
 A:Map position: 1p35-1p35

A:Intons: 32/1, 147/3, 222/1, 264/1, 403/1, 454/1, 481/1
 C:Complex: homotrimer

C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat
 C:Keywords: glycoprotein; homotrimer

F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-496/Product: cartilage matrix protein #status predicted <MAT>

F:39-206/Domain: von Willebrand factor type A repeat homology <VMA1>
 F:227-262/Domain: EGF homology <EGF>

F:273-437/Domain: von Willebrand factor type A repeat homology <VMA2>
 F:76,344/Binding site: carbohydrate (asn) (covalent) #status predicted

F:221-238,234-247,249-262/Disulfide bonds: #status predicted
 Query Match 14.3%; Score 501.5; DB 2; Length 496;
 Best Local Similarity 28.8%; Pred. No. 8.9e-26;

Matches 129; Conservative 80; Mismatches 178; Indels 61; Gaps 9;

QY 273 EELSTQSLFVSLGDPNCK---IDLSEFLIDGSTSIGKRRFRIOKQLADVAQALDIGPAG 329
 Db 19 QALCSPELAPQSRGH-LCRRRPDILVAVDSSSVRVEFEKVKVFLSQVIESLDVGRNA 77
 QY 330 PLMGVGYDGNPAPHILKTHNSRDILTAIEKTIQGGLSNVGRAISFVTKNFFSKANG 389
 Db 78 TRVGMVYASTVQKEFSLRAHVSKAALQAVRIQPLSTGMTGLAIFAITKAFGDAEG 137
 QY 390 NRSAPR---VVVVMDGWTVDVEASRLARESGINIFITIEGAENE--KQYVVEPN 444
 Db 138 GRKSPDISKRVYVVDGRQDVQVDSAPARASGVELFAIGV-GSDVKAATLRQIASEPQ 196
 QY 445 FANKAVCTRTGFSLVHOSFGLHKTLP-----LVKRCVDTDLRLACSKTCLNS----- 493
 Db 197 DEHYD-----YVESISVIEKLSRKQEAFCVSDLCAGDHCEQVCISSPSSTY 246
 QY 494 -----ADIGFVIDGSSSVGTGNFTVLQFVNTLTKEFE 526
 Db 247 CACHEGFTLSDKTCNVCSGGGSSATDLVFLIDGSKSVRPENFELVKKFISQIVDTLD 306
 QY 527 ISPTDIRIGAVQTYEQRLEFGFDKYSKPDILNAIKRVGVWSG-STGAALNEALF 586
 Db 307 VSDKLAQVGLVQVSSVRQEPFLGRPHTKDILAAVARNMSMERGTWTGAALXYLIDNSF 366
 QY 587 KKS---KPNRKMLITDGRSYDVRIPMAAHLKGVITYAIGVAAQEELEVIATHP 643
 Db 367 TVSSGARPGAQKIGVFTDGRSODYINDAKKAKDLGFKMFAVGVNAVEDELREIASEP 426
 QY 644 ARDHSFEVDEFDNLHQVPRIIQNICTE 671
 Db 427 VAHEHYFTADFKTINQKKLQKKICVE 454

RESULT 4

A33809
 cartilage matrix protein precursor - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33809; A26364
 R:Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Meubust, K.A.; Primmerger, E.; Argre, J. Biol. Chem. 264, 8126-8134, 1989

A:Title: Structure of the gene for cartilage matrix protein, a modular protein of the extrins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor. A:Reference number: A33809; MUID:89255246; PMID:2542265

A:Accession: A33809
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-493 <KIS>

A:Cross-references: UNIPROT:P05099; UNIPARC:UPI00004F1EF; GB:X12346; GB:X12347; GB:X123.
 R:Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetlinck, P.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
 A:Title: Structural features of cartilage matrix protein deduced from cDNA.

A:Reference number: A26364; MUID:87092429; PMID:3025875
 A:Accession: A26364

A:Molecule type: mRNA
 A:Residues: 78-493 <ARG>

A:Cross-references: UNIPARC:UPI000004F1EF; GB:M14792; NID:9211545; PIDN:AAA48695.1; PID:
 C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat

F:37-204/Domain: von Willebrand factor type A repeat homology <VMA1>
 F:225-260/Domain: EGF homology <EGF>

F:270-434/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 14.0%; Score 490; DB 2; Length 493;
 Best Local Similarity 29.6%; Pred. No. 5.2e-25;
 Matches 155; Conservative 68; Mismatches 177; Indels 52; Gaps 7;

QY 293 DLSFLIDGSTSIGKRRFRIOKQLADVAQALDIGPAGLGVGVGYDGNPAPHILKTHN 352
 Db 39 DLFVITDSRSVRPQGEKVKVFLSVIEGLDVGPRSTRVGIVNYSARKNESLKTHTQ 98
 QY 353 SRDLTAIEKTIQGGLSNVGRAISFVTKNFFSKANGRSAPN---VVVVMDGWPPTDK 409

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Db      99 KAEILQVQRIEPLSTGTMTGLAIQFAISRAFSDEGARLRSPINKVAIVTDGRPDG 158
Qy      410 VEEASRIARSSGINIFL-----TIGGAENENQYVEENFANK---AV 450
Db      159 VQDSARARQAGLEIFAIGVRDMHTLRQIASPELDDHVDVESYVIEKLTTHKFOEAF 218
Qy      451 C-----RTNGFYSLHVQSWFGIAHKTLOPLVGRVCDTRLACSKTCLN 492
Db      219 CVVSDLCATGDHDEQICITSPGSYKCACKEGFLNND-----GKTS-----ACSGSSGS 269
Qy      493 SADIGFVIDSSSVGTGNFRTVLQFTNLKEFEISDTDRIGAVQYTYEQRLFEGDKY 552
Db      270 ALDLVFLIDGSKSVRPENFELVKKFIIQIVESLEVSSEKQAVQVYSSSVROEPLPGQF 329
Qy      553 SSKRDLINAIKRVGWSGSGTGAINPALEQLF---KKSPNKRKMLITDGRSYDV 609
Db      330 KKKKDIKAAVKKAAVMEKGTWTGALKLVDSFSISANGAPGVKGVITDSDYI 389
Qy      610 RIPMAAHLKGVITYAIGVMAAOELEVIAHPARDHSFVDFDNLHOVPRRIIONIC 669
Db      390 TDAKAKKADIGFRNFAVGVGAVIDELREIASEVVAHYFYTADFRTISNIGKKLQMKIC 449
Qy      670 TE 671
Db      450 VE 451

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RESULT 5

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566522
cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Azodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Haripi, L.; Boese, Z.
Eur. J. Biochem. 236, 970-977, 1996
A/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <AS2>
A/References: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035; NID:g1163178; PI
C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-500/Product: cartilage matrix protein #status predicted <MAT>
F:43-210/Domain: von Willebrand factor type A repeat homology <VMA1>
F:231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VMA2>

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Query March 14.0%; Score 490; DB 2; Length 500;
Best Local Similarity 28.8%; Pred. No. 5.3e-25;
Matches 130; Conservative 72; Mismatches 184; Indels 66; Gaps 8;

Qy      266 SLGLVPEEELSTQSLPEVSLDPPNCKLDLSEFLIDGSTSIGKRRFRIQKOLADVAQALDI 325
Db      27 SLISVPPQRLHLCSTRPT-----DLVFDVDSNSVRVEEKVAVFLSYLTSLDV 77
Qy      326 GPAGPLMGVOYQGNPATHEVLKTHNSRDLKTIKTIORGASINGRASIPYTKRFFS 385
Db      78 GPNAITRGLVNVASTVKEPEFLRHAGSKASLQAVRRIOPLSTMTMGLAQFRTIALS 137
Qy      386 KANGNRGAPV---VVVVMDVGMPTDKVEASRLARBSGINIFITTEGAENK---KQYV 440
Db      138 DABGRARSPDISKVIIVTDGRPODSVRDVSERARSGLELFAIGL-GRVDAKTLRQIA 196
Qy      441 VEPNFAKAVCRITNGFYSLHVQSWFGIAHKTLOP-----LVKRVCDTRLACSKTCLNS 493
Db      197 SEPDEHDV-----YESINVIKLAKKRQAEFCVVSDDCAIGDHDCBGLCVSSP 246
Qy      494 -----ADIGFVIDSSSVGTGNFRTVLQFTNL 522

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Db      247 GSYTCACHBGFLLNSDGTCTWCRGGSSGASATDLVFLIDGSKSVRPENELVKKFINQIV 306
Qy      523 KEFEISDTDRIGAVQYTYEQRLFEGDKSSKPDILNMIKRVGWSGSGTGAINPAFL 582
Db      307 DTLVDSDRLAQVGLVQVYSSIRQEPFLGRFHSKDDIKAVRNMSYVEKGTMTGAALKYLI 366
Qy      583 EQLFKS---KPKRKRLMLITDGRSYDVRIPMAAHLKGVITYAIGVMAAOELEVY 639
Db      367 DNSFTYSSGARPPAQGVIGVITDGRSDYIINDARAKOLGFRMFAVGVGNVVEELREI 426
Qy      640 AHPARDHSFVDFDNLHOVPRRIIONICTE 671
Db      427 ASEPVADHYFYTADFRTINQIGKKLOKQICVE 458

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RESULT 6

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CGH03A
collagen alpha 3(VI) chain precursor [validated] - human
N/Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 16-Aug-2004
C/Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S48
R/Chu, M.L.
submitted to Genbank, May 1998
A/Reference number: A59140
A/Accession: A59140
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3176 <CHU>
A/Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126DAF; GB:X52022; NID:g3127925; PIDN:
R/Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.J.; Glatville, R.; Maye
EMBO J. 9, 385-393, 1990
A/Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
itors
A/Reference number: S13679; MUID:90151612; PMID:1689238
A/Accession: S13679
A/Molecule type: mRNA
A/Residues: 1-30,237-313, 'CW', 318-322, 'AR', 326-1815, 'FD', 1818-1819, 'ID', 1822-3176 <CH5>
A/Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
A/Accession: S24465
A/Molecule type: protein
A/Residues: 574-585;965-973, 'X', 975-976;1306-1325;1361-1377;1381-1401;1473-1506, 'X', 1508
-1962, 'X', 1964-1965;2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X', ;
A/Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
CIC, UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C1E; UNIPARC:UPI0000173C1F; UNIPARC:UPI0000
10000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C27
R/Zanussi, S.; Dolianna, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A/Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain s
A/Reference number: S28776; MUID:93054780; PMID:1339440
A/Accession: A57083
A/Molecule type: DNA
A/Residues: 310-328 <ZAN>
A/Cross-references: UNIPARC:UPI0000173C28
A/Accession: S28776
A/Molecule type: mRNA
A/Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZAN>
A/Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AB24261.1; PID:5
R/Chu, M.L.; Mann, K.; Deutzmann, R.; Pithula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.;
Eur. J. Biochem. 168, 309-317, 1987
A/Title: Characterization of three constituent chains of collagen type VI by peptide seq
A/Reference number: S00126; MUID:88029444; PMID:3665927
A/Accession: S00245
A/Molecule type: mRNA; protein
A/Residues: 2024-2046;2092-2156, 'R', 2203-2208, 'X', 2210-2211, 'X', 2213-2227;2228-2251;22314
A/Cross-references: UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A;
ID:91335034
A/Note: the mRNA portion of the sequence corresponds to residues 2092-2157
R/Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R.
J. Biol. Chem. 263, 18601-18606, 1988
A/Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
A/Reference number: A31952; MUID:89066644; PMID:3198591

```

A:Accession: C31952
 A:Molecule type: mRNA
 A:Residues: 2038-2373 <CH4>
 A:Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
 A:Note: parts of this sequence were determined by protein sequencing
 R.Well, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, D.; Mann, K.; Deutz
 Am. J. Hum. Genet. 42, 445-445, 1988
 A:Title: Cloning and chromosomal localization of human genes encoding the three chains of
 A:Reference number: A29848; MUID:88161046; PMID:3348212
 A:Accession: C29848
 A:Molecule type: mRNA
 A:Residues: 2092-2151 <WET>
 A:Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:G291919; PIDN:AAAS2057.1; PID:
 A:Note: part of this sequence was determined by protein sequencing
 R.Jander, R.; Rautenberg, J.; Gnanville, R.W.
 Eur. J. Biochem. 133, 39-46, 1983
 A:Title: Further characterization of the three polypeptide chains of bovine and human st
 A:Reference number: 826506; MUID:83209648; PMID:685203
 A:Accession: 826510
 A:Molecule type: protein
 A:Residues: 'SAIAGVAGV' <JAN>
 A:Cross-references: UNIPARC:UPI0000173C2F
 A:Note: this sequence cannot be reliably placed and probably represents the results from
 R.Meyer, U.; Poeschl, E.; Nisch, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 225, 573-580, 1994
 A:Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor mod
 A:Reference number: 548709; MUID:95045506; PMID:7525281
 A:Accession: 548709
 A:Molecule type: mRNA
 A:Residues: 'MMAWIFLITACGALAA', 3102-3176 <MAY>
 A:Cross-references: UNIPARC:UPI0000173C30
 A:Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor h
 R.Arnoux, B.; Merigau, K.; Saladjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O.;
 submitted to the Brookhaven Protein Data Bank, August 1994
 A:Reference number: A52812; PDB:1KNT
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160
 A:Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 sines are 5-hydroxylated and subsequently O-glycosylated.
 C:Comment: The fibronectin type III repeat homology domain may be released during proces
 C:Genetics:
 A:Gene: GDB:COL6A3
 A:Cross-references: GDB:119066; OMIM:120250
 A:Map position: 2937.3-2937.3
 C:Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGH1JA),
 sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
 C:Function:
 A:Description: structural component of extracellular tissue microfibrils associated with
 C:Superfamily: collagen VI
 C:Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; extracel
 F:1-25/Domin: signal sequence #status predicted <SIG>
 F:26-3176/Product: collagen alpha 3(VI) chain #status predicted <MNT1>
 F:26-2037/Domin: amino-terminal nonhelical #status predicted <ANH>
 F:26-30,237-3176/Product: collagen alpha 3(VI) chain, splice form A9/N10(-) #status pred
 F:37-203/Domin: von Willebrand factor type A repeat homology <W01>
 F:240-405/Domin: von Willebrand factor type A repeat homology <W02>
 F:443-608/Domin: von Willebrand factor type A repeat homology <W03>
 F:637-602/Domin: von Willebrand factor type A repeat homology <W04>
 F:835-999/Domin: von Willebrand factor type A repeat homology <W05>
 F:1027-1191/Domin: von Willebrand factor type A repeat homology <W06>
 F:1331-1394/Domin: von Willebrand factor type A repeat homology <W07>
 F:1434-1599/Domin: von Willebrand factor type A repeat homology <W08>
 F:1537-1802/Domin: von Willebrand factor type A repeat homology <W09>
 F:1836-2005/Domin: von Willebrand factor type A repeat homology <W10>
 F:2038-2373/Region: interrupted helical
 F:2040-2042/Region: cell attachment (R-G-D) motif
 F:2136-2138/Region: cell attachment (R-G-D) motif
 F:2148-2150/Region: cell attachment (R-G-D) motif
 F:2154-2156/Region: cell attachment (R-G-D) motif
 F:2370-2372/Region: cell attachment (R-G-D) motif
 F:2374-3176/Domin: carboxyl-terminal nonhelical #status predicted <CNH>
 F:2400-2571/Domin: von Willebrand factor type A repeat homology <W11>
 F:2617-2800/Domin: von Willebrand factor type A repeat homology <W12>

F:2665-2986/Region: alanine/lysine/proline/threonine/valine-rich repeats
 F:2987-3072/Domin: fibronectin type III repeat homology <FN3>
 F:3111-3161/Domin: animal Kunitz-type proteinase inhibitor homology <API>
 F:316/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted
 F:108,116,202,251,2079,2331,2558,2677,2681,3036/Binding site: carbohydrate (Aan) (covale
 F:2087/Disulfide bonds: interchain #status predicted
 F:2100,2206,2239,2316,2319/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:2103,2209,2212,2322,2337/Binding site: carboxylate (Lys) (covalent) #status experi
 F:2103,2209,2212,2322,2337/Modified site: 5-hydroxylysine (Lys) #status experimental
 F:3111-3161,3120-3144,3136-3157/Disulfide bonds: #status predicted
 Query Match 13.58; Score 471.5; DB 2; Length 3176;
 Best Local Similarity 30.95; Pred. No. 1.5e-22;
 Matches 122; Conservative 86; Mismatches 148; Indels 39; Gaps 12;
 Oy 293 DLSFLIGSTSGRRRIKOLLADVAOLDGPAPGLMGVQYGDGNPATHTLKTHTN 352
 Db 39 DIFPLVSSWTIGEHFQVREFLVDVVASLAVGENDFHFLVQNGNPHTLELTIRT 98
 Oy 353 SRDLKTAIEKITRGSLNVGRAISFVTKNPFKANGNR--GAPNVVVMVDGMPPTKV 410
 Db 99 KQVLSHISMSYIGTNGQKLEVIYMSHLTKAAGSRAGDVPQYIVVLTGHSKDGL 158
 Oy 411 EASRLARESGINIFFTTGAANE-KQYVEPNFANKAVCTRTGFSYH--VQSMFG- 466
 Db 159 ALPSAEIKSADVNVFAIGVADGALKEIASEP--LNMFMFULENFTSLHDIQNLVSC 216
 Oy 467 LKHTLOPLVRCDDPRLACSKTCLNSADIGFPIIDSSVGTGNFRVLQFVNTLKEFE 526
 Db 217 VHSVSP--ERAGDTLTK-DITAGDSADITFLIDSSNNTGVSFAVILDFLVNLEKLP 273
 Oy 527 ISDTRIGAVQYTYEQREFGFQKYSKPDILNAIKRVGWSGG--TSTGAINFALQ 584
 Db 274 IGQQRGVGVQSDERTMFSLDYSTKQVGVAGVAGLF-AGGELANIGLALDFVEN 332
 Oy 585 LFKKSKPNK-----RKLMTITDGRSYDVRIPAMAHLKGVITYTVAIGVMAAOELEVI 639
 Db 333 HFRAGGSRVEEGVPOVLVISAGPSSDEIRYGVVALKQASVPSFGIGQAASRAELQHI 392
 Oy 640 ATRPARDSFVDFPNLQYVRIIONTCEENS 674
 Db 393 ATD-----DNLVFTVP-----EPRS 407
 RESULT 7
 S31212
 collagen alpha 1(XIV) chain precursor, short form - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Mar-1998 #revision 17-Apr-1998 #text_change 15-Sep-2003
 C:Accession: S31212
 R:McElchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
 Eur. J. Biochem. 212, 483-490, 1993
 A:Title: Complete primary structure of chicken collagen XIV.
 A:Reference number: S31211; MUID:931855668; PMID:8444186
 A:Accession: S31212
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1857 <WAP>
 A:Cross-references: UNIPARC:UPI000017123C; EMBL:X70792; NID:G288874; PIDN:CAAS0063.1; PIR:
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C:Genetics:
 A:Gene: COL14A1
 C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer;
 F:1-28/Domin: signal sequence #status predicted <SIG>
 F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
 F:29-110/Domin: fibronectin type III repeat homology <FN3A>
 F:156-320/Domin: von Willebrand factor type A repeat homology <WNA1>
 F:352-433/Domin: fibronectin type III repeat homology <FN3B>
 F:442-525/Domin: fibronectin type III repeat homology <FN3C>
 F:534-614/Domin: fibronectin type III repeat homology <FN3D>
 F:623-107/Domin: fibronectin type III repeat homology <FN3E>
 F:741-823/Domin: fibronectin type III repeat homology <FN3F>
 F:832-914/Domin: fibronectin type III repeat homology <FN3G>

F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 331; DB 2; Length 1857;
Best Local Similarity 24.8%; Pred. No. 1,66-13;

Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

Qy 174 ICGTAQPTVLMQLAVTVAAPTLLPPSPSAASTSIIPROSQVHRSQEMD----- 227
Db 713 ICGTAAPT-----VTTTTTATTPKPTIAVFRT-----GVRLVVIDDETTSS 757
Qy 228 ---LMSATYTSQNR-----PRADPGIORODPSGAAPQKPVGADVSLGLVPEELS 276
Db 758 LRVVMDISDHNAQCFRTVTLTAKGDRAEBAIMVPGQNTLLIQP-----LLPDEYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDSLFIDGSTSIGKRRFRIOQLADVAQALDGPAGP 330
Db 810 VTTPIYADGEGVSAPGKTLPLS-----APRLRVSDSEWNRRLISWD-APSP 859
Qy 331 LMG--VVOYGDN---PATFNLKTHNSRDLKTAIEKITQRGSLSVGRLAISVTKNFP 385
Db 860 TWGRIYKSIINPGPA---LETFVGD-DINTL-----ILNLFSGTEYSVAVFAS 906
Qy 386 KANG---NRSGAPNVVVVWDGWPDKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTVAKTLYLGVTNLDYQVRMTSLCAQWQLRHATAVRVVIESLVDEKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTQ----- 472
Db 966 --EVNLGG-GVPR-HCFEFLMPGTEYKISVHQAQLEIEGPVAVSIMETTLPPPTQPTSP 1021
Qy 473 -----PLVKRVCPTDLACSKTCLNSADIGFVIDSSSVGTGNRTVLQPVNTLTK 524
Db 1022 TLLPPTIPPAKEVCAAK-----ADLVFLVDGWSISGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTRIGAVQYVEQRLEFGPKYSKPDILNAIKRVGWSGCTSTGAINFAL 583
Db 1072 LDKIGPDGTQVALIQSDDPRTFELKNAVKTKETLLLEAIQQLAYKGNTKTGAKIGHAR 1131
Qy 584 QLF-----KSKPKNRKMLILITDGRSYDDVRIPMAAHLKVITYAIGVMAAOEEL 637
Db 1132 VLFTGEAGMRKGIIP---KVLVITIDGRSQDDVKNVKSREMQLDGFSPFALGVADADYSELV 1188
Qy 638 VIATHPARDSFVDEFDNLHQVPRILIONIC 669
Db 1189 NIGSKPSERHVFVDPDFDAFTKIEDELITFVC 1220

RESULT 8

S78476 collagen alpha 1(XIV) chain precursor, long form - chicken
C/Species: Gallus gallus (chicken)
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S78476; S31211
R/Trueb, B.
submitted to the EMBL Data Library, January 1993
A/Reference number: S78476
A/Accession: S78476
A/Molecule type: mRNA
A/Residues: 1-1888 <TRU>
A/Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:S288872; PII
R/Welchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A/Title: Complete primary structure of chicken collagen XIV.
A/Reference number: S31211; MUID:93185668; PMID:8444186
A/Accession: S31211
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-415;1460-1811,1843-1888 <MAE>
A/Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
C/Genetics:
A/Gene: Col14A1
C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime

F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;632-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 331; DB 2; Length 1888;
Best Local Similarity 24.8%; Pred. No. 1,76-13;

Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

Qy 174 ICGTAQPTVLMQLAVTVAAPTLLPPSPSAASTSIIPROSQVHRSQEMD----- 227
Db 713 ICGTAAPT-----VTTTTTATTPKPTIAVFRT-----GVRLVVIDDETTSS 757
Qy 228 ---LMSATYTSQNR-----PRADPGIORODPSGAAPQKPVGADVSLGLVPEELS 276
Db 758 LRVVMDISDHNAQCFRTVTLTAKGDRAEBAIMVPGQNTLLIQP-----LLPDEYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDSLFIDGSTSIGKRRFRIOQLADVAQALDGPAGP 330
Db 810 VTTPIYADGEGVSAPGKTLPLS-----APRLRVSDSEWNRRLISWD-APSP 859
Qy 331 LMG--VVOYGDN---PATFNLKTHNSRDLKTAIEKITQRGSLSVGRLAISVTKNFP 385
Db 860 TWGRIYKSIINPGPA---LETFVGD-DINTL-----ILNLFSGTEYSVAVFAS 906
Qy 386 KANG---NRSGAPNVVVVWDGWPDKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTVAKTLYLGVTNLDYQVRMTSLCAQWQLRHATAVRVVIESLVDEKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTQ----- 472
Db 966 --EVNLGG-GVPR-HCFEFLMPGTEYKISVHQAQLEIEGPVAVSIMETTLPPPTQPTSP 1021
Qy 473 -----PLVKRVCPTDLACSKTCLNSADIGFVIDSSSVGTGNRTVLQPVNTLTK 524
Db 1022 TLLPPTIPPAKEVCAAK-----ADLVFLVDGWSISGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTRIGAVQYVEQRLEFGPKYSKPDILNAIKRVGWSGCTSTGAINFAL 583
Db 1072 LDKIGPDGTQVALIQSDDPRTFELKNAVKTKETLLLEAIQQLAYKGNTKTGAKIGHAR 1131
Qy 584 QLF-----KSKPKNRKMLILITDGRSYDDVRIPMAAHLKVITYAIGVMAAOEEL 637
Db 1132 VLFTGEAGMRKGIIP---KVLVITIDGRSQDDVKNVKSREMQLDGFSPFALGVADADYSELV 1188
Qy 638 VIATHPARDSFVDEFDNLHQVPRILIONIC 669
Db 1189 NIGSKPSERHVFVDPDFDAFTKIEDELITFVC 1220

RESULT 9

A54849 collagen alpha 1(VII) chain precursor - human
N/Alternate names: procollagen alpha 1(VII) chain
C/Species: Homo sapiens (man)
C/Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C/Accession: A54849; S16316; S16318; S16328; A30286; I84686
R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Utico, J.
J. Biol. Chem. 269, 20256-20262, 1994
A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VII)
A/Reference number: A54849; MUID:94337588; PMID:8051117
A/Accession: A54849
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-2944 <CHR>

A:Cross-references: UNIPROT:002388; UNIPARC:UPI000017A138; GB:L02870; NID:G987124; PIDN: R.Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A:Title: Molecular cloning and characterization of type VII collagen cDNA.
A:Reference number: P10844; MUID:92231902; PMID:1567409
A:Accession: P10844
A:Molecule type: mRNA
A:Residues: 'EPR', 340-475, 'ALSTASHSTLCWRATRMHPCNRGSHWTRACPCNRPASHPARAG', 524-528, 'C',
A:Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:G453698; PIDN: E
A:Experimental source: keratinocyte
A:Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R.Parente, M.G.; Chung, L.C.; Rymmenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mac
Proc. Natl. Acad. Sci. U.S.A. 86, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
A:Accession: S16316
A:Molecule type: mRNA
A:Residues: 815-892, 'E', 894-1439 <PAR>
A:Cross-references: UNIPARC:UPI000016A722; GB:M65158; GB:S49017; NID:G180914; PIDN:AAA96
A:Experimental source: keratinocyte
R.Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Priyaanah, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A:Reference number: 156328; MUID:93107742; PMID:1469284
A:Accession: 156328
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'EPR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A:Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:G262308; PIDN:AA24637.1; PID:
J. Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgess, R.E.
J. Biol. Chem. 264, 3822-3828, 1989
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagenase
A:Reference number: A30296; MUID:89139437; PMID:2537292
A:Accession: A30296
A:Molecule type: Protein
A:Residues: 'AY', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 2032, 'C', 2034-2041, '
A:Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A:Note: two reported peptides cannot be reliably located
R.Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: 148103; MUID:9271985; PMID:8499916
A:Accession: 148103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2395-2871, 'S', 2873-2944 <RE2>
A:Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:
R.Christiano, A.M.; Rymmenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A:Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub
A:Reference number: A55255; MUID:94224777; PMID:8170945
A:Contents: annotation
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL7A1; EBR1; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring f
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproli
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>
F:36-201/Domain: von Willebrand factor type A repeat homology <WVA1>
F:231-318/Domain: fibronectin type III repeat homology <FN1>
F:337-413/Domain: fibronectin type III repeat homology <FN2>
F:414-502/Domain: fibronectin type III repeat homology <FN3>
F:508-593/Domain: fibronectin type III repeat homology <FN4>
F:598-683/Domain: fibronectin type III repeat homology <FN5>

F:686-771/Domain: fibronectin type III repeat homology <FN6>
F:776-862/Domain: fibronectin type III repeat homology <FN7>
F:864-992/Domain: fibronectin type III repeat homology <FN8>
F:954-1045/Domain: fibronectin type III repeat homology <FN9>
F:1052-1219/Domain: von Willebrand factor type A repeat homology <WVA2>
F:1170-1172/Region: cell attachment (R-G-D) motif
F:1189-1253/Region: cysteine/proline-rich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2253-2555/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F:2876-2929/Domain: animal knittz-type proteinase inhibitor homology <BPI>
F:337,786,1109/Binding site: carbohydrate (asn) (covalent) #status predicted
F:2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status exper
F:2625,2631/Modified site: 5-hydroxylysine (lys) #status experimental
F:2625,2631/Binding site: carbohydrate (lys) (covalent) #status experimental
F:2654,2802,2804/Disulfide bonds: interchain #status predicted

Query Match 9.4%; Score 329.5; DB 2; Length 2944;
Best Local Similarity 35.7%; Pred. No. 4.1e-13;
Matches 80; Conservative 37; Mismatches 86; Indels 19; Gaps 4;

Qy 470 TLDPYKRV-----DTRLACSKTCLNSADIGFYIDSSVGTGNFTVLO 516
Db 2 TLRLVALCAGILAEAPRVRAQHRRERVCTTR--LYADIVFLDSSISGRSFRVRS 59
Qy 517 FVNTNLTKEFE--ISDIDTRIGAOYTYEQLLEGFDKSKRPILNAIKRVGVSGGTST 574
Db 60 FLSELVLPFGAASAOQVRATVQYSDPTEFGDLGSGGVDTAIRIRLSYKSGNTRT 119
Qy 575 GAAMFALAEOLF--KSKPKMKRLMLITDGRSDVDRIAPMAAHLGVTVAIGVMAA 632
Db 120 GAAMLHVAHDVFLPQLARPEVPVVCILITDGSQODLVDTAAQGLKGGVGLFANGIQAD 179
Qy 633 QESLEVIATIPADHSFVDEPNLHOYPRITQNTCTEFSNP 676
Db 180 PEEKIRVASOPTSDFFEFVNDPFSILRLTLPVLRVCTTAGVP 223

RESULT 10
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N:Alternate names: undulin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A45974; S30085; S22916; S17035; S20833
J.Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lina
J. Biol. Chem. 268, 12177-12184, 1993
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' regions
A:Reference number: A45974; MUID:93280195; PMID:8505337
A:Accession: A45974
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-1747 <GER>
A:Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47
A:Experimental source: embryo skin
A:Note: sequence inconsistent with the nucleotide translation
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30085
A:Molecule type: mRNA
A:Residues: 1472-1660 <APT>
A:Cross-references: UNIPARC:UPI0000006A2; EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:
R. Trubel, J.; Trubel, B.
Eur. J. Biochem. 207, 549-557, 1992
A:Title: Type XIV collagen is a variant of undulin.
A:Reference number: S22916; MUID:92339443; PMID:1339349
A:Accession: S22916
A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'K', 1122-1402, 1409-1439 <TRU>
 A:Cross-references: UNIPARC:UPI0000173C48
 R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsemayer, T.F.; van der Rest, M.; Mayne, B.; U. Blochem. 201, 333-338, 1991
 A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
 A:Reference number: S17035; MUID:92037585; PMID:1935930
 A:Accession: S17035
 A:Molecule type: mRNA
 A:Residues: 1472-1659 <GOR1>
 A:Cross-references: UNIPARC:UPI0000173C49
 A:Accession: S20833
 A:Molecule type: protein
 A:Residues: 1551-1570, 1593-1639-1667 <GOR2>
 A:Cross-references: UNIPARC:UPI0000173C49
 C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
 F:40-204/Domain: von Willebrand factor type A repeat homology <WMA1>
 F:236-317/Domain: fibronectin type III repeat homology <FN3A>
 F:336-409/Domain: fibronectin type III repeat homology <FN3B>
 F:418-498/Domain: fibronectin type III repeat homology <FN3C>
 F:507-591/Domain: fibronectin type III repeat homology <FN3D>
 F:625-707/Domain: fibronectin type III repeat homology <FN3E>
 F:716-798/Domain: fibronectin type III repeat homology <FN3F>
 F:806-893/Domain: fibronectin type III repeat homology <FN3G>
 F:924-1089/Domain: von Willebrand factor type A repeat homology <WMA2>
 F:1111-1353/Domain: non-collagenous NC4 #status predicted <NC4>
 F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
 F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 9.4%; Score 329; DB 2; Length 1747;
 Best Local Similarity 24.8%; Pred. No. 2e-13;
 Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

Qy 174 IPGTTAOPVTLMLAATVAVATPTLPSPSPSAATSTSIIPQSVGHRSGEMD----- 227
 Db 597 IVGTTAIPPT-----VTTTATTPKPTIAVFR-----GVRLVVIDETSS 641
 Qy 228 ---LMSATATYSQNR-----PRADPGIORODPSGAAPQKVGADVSLGLVPKEELS 276
 Db 642 LRVVWMDISDHAQOFRTYTLAKGDRABEAIMVPRGRQNTLLQP-----LLPDEYK 693
 Qy 277 TQSL-----EPVSLGPNCKIDSLFDGSTSGKRRFRIOQLADVAQALDIDGAP 330
 Db 694 VITPIYADEGVSAAGKTLPLS-----APNLRVSDVMYRLISWD-APPSP 743
 Qy 331 LMG--VVQYGDN---PATFHLKHTNSRDLKTAIEKITORGGLSNVGRASIFVTKNFFS 385
 Db 744 TMGRIVYKSLNVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVKVPAS 790
 Qy 386 KANG---NRSGAPNVVVVWDGMPDKVEASRLAR--BSGINIFPITTEGAENKQY 439
 Db 791 YSTGFSDALGVAKTYLIGVTNLDYQVRMTSLCAQOQLRHNRHATRVVIVESLVDGKO- 849
 Qy 440 VVENPANKAVCRNGFYSL--HYQSWFGLHKTLO----- 472
 Db 850 --EVNLGG-GVPR-HCFEELMPGTEYKISVHAQOELEGPAVSIMETTLPPPTOPS 905
 Qy 473 -----PLVKRVCDTDLRACSTKCLNSADIGVIGSSSVGTGNFRVTLQFVNTLKE 524
 Db 906 TTLPPPTIPPAKCYCAK-----ADLVFVVGSMISGDNDNKIISFLYSVGA 955
 Qy 525 FE-ISTDTRIGAVQYTYEORLEFGFDKYSKSPDILNAIKRVGWSGSGTGAALNFALE 583
 Db 956 LDKIGPGTQVALIOLFSDPRTPEKLANVYKTEKTELLBAIQIAVKGNTKTKAIKARE 1015
 Qy 584 QLF-----KSKRNKRLMLITDGRSYDVRIPMAAHLKVITTAIGVAMAQOELE 637
 Db 1016 VLTFGAGMRKGI--KVLVITDGRSODDVNVKVSREMOLDGSSFFAIGVADYSELV 1072
 Qy 638 VIATHPARDSFVDEFDNLHOVPRITONIC 669
 Db 1073 NIGSKPSERHVFVDDDAFKIDELELITFVC 1104

RESULT 11
 T28797
 hypothetical protein C16E9.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #ext_change 09-Jul-2004
 C:Accession: T28797
 R:Geisler, C.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C16E9.
 A:Reference number: Z20525
 A:Accession: T28797
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-567 <GE1>
 A:Cross-references: UNIPROT:Q18048; UNIPARC:UPI000007FC64; EMBL:U93677; P1DN:AAC47957.1;
 A:Experimental source: strain Bristol N2; clone C16E9
 C:Genetics:
 A:Gene: CESP.C16E9.1
 A:Map position: X
 A:Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1

Query Match 9.0%; Score 314.5; DB 2; Length 567;
 Best Local Similarity 22.0%; Pred. No. 3.5e-13;
 Matches 130; Conservative 84; Mismatches 213; Indels 163; Gaps 20;

Qy 172 PPIPGTTAOPVTLMLAATVAVATPTLPSPSPSAATSTSIIPQSVGHRSGEMDLS 230
 Db 37 PMP-----PTDPPGVDPDTPPTTPPRAPPSGLAPRPMKMT 75
 Qy 231 TATYSSQNR-----RADPGIORODPSGAAPQKVGADVSLGLVPKEELSTQSL 280
 Db 76 QEIPKSSGQQLKIEDVVVGNNDISHVEEVNGSGSDTSGSGSGDSCGTEESFDASGEA 135
 Qy 281 EPIVSLD-----PNCKIDSLFDGSTSGKRRFRIOQLADVAQALDIDG 327
 Db 136 QGDSLDPIMKAMDSEAVLGVNCPDITFVIDTSSV-KGIFQYTYIEKVEGADVDP 194
 Qy 328 AGPLMGVQYGD--NPATFHLKHTNSRDLKTAIEKITORGGLSNVGRASIFVTKNFFS 385
 Db 195 TVDHVGAIVYSSSEKRTIKLGEHKDRGSIVAVDELFPFGSITNTGALKRPAANH----- 251
 Qy 386 KANGNSGAPNVVVVWDGMPDKVEASRLARBSGINIFPITTEGAENKQYVVENP 445
 Db 252 -TEGRENEFTLVNVIITDGSYDLIESGARVIRE-----VPSN 288
 Qy 446 ANKAVCRNGFYSLHYQSWFGLHKTLO-----PLVGR--VCDT----- 481
 Db 289 A-----IYAVSIGEIF-LKKELEMITGNPDNVLTGSMSTGYLVKRLKLCDAIRAKA 338
 Qy 482 -----DRLACS-----KTCLNSADIGF 498
 Db 339 TLKDSNPLGVPRPEFLSDRFQHRSLTANLEAKKHEDFVKPEKRPYKDC--YDIG 396
 Qy 499 VIDSSSVGTGNFRVTLQFVNTLKEFEISDTRIGAVQYTYEORLEFGFDKYSKSPDI 558
 Db 397 IPDSSGSL-EKMFQKQLAFKQLVBEQMPISDNAVTRGIVQFAGKTVKRVLANFSQKSL 455
 Qy 559 LNAIKRVGWSGSGTGAALNFALEQLEFKSK--PNRKMMLITDGRSYDVRIPMAAHL 617
 Db 456 KTIIDRSPFYSGITFTNOAIK-KMAALYESKRPNAKMLFTDYSIAEDTSEGEALK 514
 Qy 618 LKGVITYAIGV-----AMAAOELEVIATHPARDSFVDEFDNLHOVPR 662
 Db 515 SQGVVVVYTGISTDKSAGLNMKELRGMAT--SEHNYDSSDFADLLKHFP 562

RESULT 12
 T46488
 hypothetical protein DKFZp434J065.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #ext_change 09-Jul-2004
 C:Accession: T46488

A:Reference number: S23676; MUID:87260814; PMID:3496594
A:Accession: S23676
A:Molecule type: DNA
A:Residues: 2731-2813 <COL>
A:Cross-references: UNIPARC:UPI000014240A; EMBL:MI6945
R:Bonthron, D.; Orr, E.C.; Mitsch, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A:Reference number: A25298; MUID:87016349; PMID:3489923
A:Accession: A25298
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-2813 <BOX>
A:Cross-references: UNIPARC:UPI000017431D; EMBL:X04385
R:Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 1839-1847, 1986
A:Title: Full-length von Willebrand factor (VWF) cDNA encodes a highly repetitive protei
A:Reference number: A91044; MUID:87004550; PMID:3019665
A:Accession: A25469
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
A:Cross-references: UNIPARC:UPI000017431C; EMBL:X04146
A:Note: this sequence has been revised in reference A91056
R:Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 3074, 1986
A:Reference number: A91056
A:Accession: A25366
A:Molecule type: mRNA
A:Residues: 1021-1030 <VE2>
A:Cross-references: UNIPARC:UPI000017431D
A:Note: this is a revision to the sequence from reference A91044
R:Shelton-Inioes, B.B.; Brose Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated
A:Reference number: S23618; MUID:87213253; PMID:3495266
A:Accession: S23618
A:Molecule type: mRNA
A:Residues: 1-120 <SH2>
A:Cross-references: UNIPARC:UPI000016830A; EMBL:M17588; NID:G799330; PIDN:AAA65940.1; PI
A:Accession: S23645
A:Molecule type: protein
A:Residues: 23-56 <SH3>
A:Cross-references: UNIPARC:UPI000017431E
R:Sadler, J.E.; Shelton-Inioes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact
A:Reference number: A94060; MUID:86016708; PMID:2864688
A:Accession: A94060
A:Molecule type: mRNA
A:Residues: 'WA', '739', 'C', '744-769', 'H', '771-788', 'A', '790-803', 'S', '805-873', '1289-1471', 'D', '1473-
A:Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320
A:Note: the authors translated the codon TCG for residue 2168 as Cys
R:Shelton-Inioes, B.B.; Titani, K.; Sadler, J.E.
Biochemistry 25, 3164-3171, 1986
A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc
A:Reference number: A90504; MUID:86265894; PMID:3488076
A:Accession: A90504
A:Molecule type: mRNA
A:Residues: 781-788, 'A', '790-1424 <SHE>
A:Cross-references: UNIPARC:UPI0000174321
R:Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; C
Science 228, 1401-1406, 1985
A:Title: Human von Willebrand factor (VWF): isolation of complementary DNA (cDNA) clones
A:Reference number: A44178; MUID:85244588; PMID:3874428
A:Accession: A44178
A:Molecule type: mRNA
A:Residues: 2621-2813 <GIN>
A:Cross-references: UNIPARC:UPI0000168307; EMBL:K03028; NID:G340308; PIDN:AAA61293.1; PI
R:Verweij, C.L.; de Vries, C.J.M.; Dieckel, B.; van Zonneveld, A.J.; van Kessel, A.G.; va
Nucleic Acids Res. 13, 4699-4717, 1985
A:Title: Construction of cDNA coding for human von Willebrand factor using antibody prob
A:Reference number: S07363; MUID:85265603; PMID:3875078
A:Accession: S07363

A:Molecule type: mRNA
A:Residues: 2731-2813 <VE3>
A:Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:G37939; PIDN:CAA26503.1; PID
R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Lang, E.H.; Living
Cell 41, 49-56, 1985
A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a r
A:Reference number: S23678; MUID:85201687; PMID:3873280
A:Accession: S23678
A:Molecule type: mRNA
A:Residues: 2731-2813 <LYN>
A:Cross-references: UNIPARC:UPI000014240A; EMBL:X03028
R:Titani, K.; Kumar, S.; Tskio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;
Biochemistry 25, 3171-3184, 1986
A:Title: Amino acid sequences of human von Willebrand factor.
A:Reference number: A90505; MUID:86269895; PMID:3524673
A:Accession: A90505
A:Molecule type: protein
A:Residues: 764-788, 'A', '790-1471', 'D', '1473-2813 <TTT>
A:Cross-references: UNIPARC:UPI0000174322
A:Note: 789-Thr was also found
R:Chopek, M.W.; Gilma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
A:Title: Human von Willebrand factor: a multivalent protein composed of identical subunit
A:Reference number: A23464; MUID:86269892; PMID:3015199
A:Accession: A23464
A:Molecule type: protein
A:Residues: 764-773; 2803-2813 <CHO>
A:Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324
R:Ident, J.A.; Berkowitz, S.D.; Mare, J.; Kasper, C.K.; Ruggieri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A:Title: Identification of a cleavage site directing the immunohemical detection of mole
A:Reference number: A36013; MUID:90349604; PMID:2385594
A:Accession: A36013
A:Molecule type: protein
A:Residues: 1606-1617 <DEN>
A:Cross-references: UNIPARC:UPI0000174325
R:Ray, P.O.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
Science 232, 995-998, 1986
A:Title: Propylpeptide of von Willebrand factor circulates in blood and is identical to
A:Reference number: A60913; MUID:86208144; PMID:3486471
A:Accession: A60913
A:Molecule type: protein
A:Residues: 576-590 <FAT>
A:Cross-references: UNIPARC:UPI0000174326
C:Genetics:
A:Gene: GDB:VWF
A:Cross-references: GDB:119125; OMIM:193400
A:Map position: 12p13.3-12p13.2
A:Intons: 19/1, 74/1, 108/2, 178/1, 218/3, 292/1, 333/1, 370/2, 386/1, 431/3, 478/1, 511
5/1, 1724/1, 1771/1, 1819/1, 1874/1, 1888/3, 1948/1, 2021/3, 2086/1, 2200/1, 2266/3, 2303
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von v
C:Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
F:1-22/Domain: signal sequence #status predicted <SIG>
F:32-763/Product: von Willebrand antigen II #status predicted <MA1>
F:34-386/Domain: type D repeat 1 <DD1>
F:387-745/Domain: type D repeat 2 <DD2>
F:698-700/Region: cell attachment (R-G-D) motif
F:764-2813/Product: von Willebrand factor #status predicted <MA2>
F:784-865/Domain: D' <DDD>
F:788-833, 2216-2261/Region: duplication
F:826-853, 2400-2515, 2544-2662/Region: duplication
F:842-1130, 1934-2203/Region: duplication
F:866-1241/Domain: type D repeat 3 <DD3>
F:1275-1443/Domain: von Willebrand factor type A repeat homology <VMA1>
F:1496-1654/Domain: von Willebrand factor type A repeat homology <VMA2>
F:1689-1854/Domain: von Willebrand factor type A repeat homology <VMA3>
F:1947-2295/Domain: type D repeat 4 <DD4>
F:2296-2330/Domain: type B repeat 1 <VB1>
F:2340-2365/Domain: type B repeat 2 <VB2>
F:2375-2399/Domain: type B repeat 3 <VB3>
F:2430-2497/Domain: von Willebrand factor type C repeat homology <VMA1>
F:2507-2509/Region: cell attachment (R-G-D) motif
F:2581-2647/Domain: von Willebrand factor type C repeat homology <VMA2>

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OM protein - protein search, using sw model
Run on: September 5, 2006, 20:01:58 ; Search time 199 Seconds
(without alignments)
1557.752 Million cell updates/sec

Title: US-10-063-538-34
Perfect score: 3502
Sequence: 1 MRYVLTMKSVIEMFLVL.....QYVPRITQICTEFNQSPRN 678
Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5
2589679 sege, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY66674	standard;	protein;	678	AA.	
DE	Membrane-bound protein PRO1277.					
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 3;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 2						
ID	AAU29098	standard;	protein;	678	AA.	
DE	Human PRO polypeptide sequence #75.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 4;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 3						
ID	AAB87542	standard;	protein;	678	AA.	
DE	Human PRO1277.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 4;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 4						
ID	AAB65197	standard;	protein;	678	AA.	
DE	Human PRO1277 (UNQ647) protein sequence SEQ ID NO:179.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 4;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 5						
ID	ABG95867	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein PRO1277.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 5;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 6						
ID	ABU58474	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #75.					

PN	US2003027272-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 7						
ID	ABU88022	standard;	protein;	678	AA.	
DE	Novel human secreted and transmembrane protein PRO1277.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 8						
ID	ABU84337	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein (PRO) #75.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 9						
ID	ABR66211	standard;	protein;	678	AA.	
DE	Human secreted polypeptide PRO1277, SEQ ID NO:150.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 10						
ID	ABR65601	standard;	protein;	678	AA.	
DE	Human secreted polypeptide PRO1277, SEQ ID NO:150.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 11						
ID	ABU99541	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein (PRO) #75.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 12						
ID	ABU58012	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #44.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 13						
ID	ABU59090	standard;	protein;	678	AA.	
DE	Novel human secreted or transmembrane protein PRO1277.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 14						
ID	ABU82602	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein PRO1277.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 15						
ID	ABU82780	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #75.					
PN	US2003032113-A1.					
PD	13-FEB-2003.					
Query Match		100.0%;	Score 3502;	DB 6;	Length 678;	
Best Local Similarity		100.0%;	Pred. No. 1.1e-306;			
RESULT 16						
ID	ABU89901	standard;	protein;	678	AA.	
DE	Novel human secreted and transmembrane protein PRO1277.					
PN	US2003036147-A1.					
PD	20-FEB-2003.					

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Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 17
ID ABR68150 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 18
ID ABU60521 standard; protein; 678 AA.
DE Human secreted/transmembrane protein, #69.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 19
ID ABU96203 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 20
ID ABU92634 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 21
ID ABO08711 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 22
ID ABO02763 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 23
ID ABR74917 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 24
ID ABR94679 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 25
ID ABU13903 standard; protein; 678 AA.
DE Human PRO1277 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 26
ID ABU85652 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 27
ID ABU98812 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 28
ID ABU98027 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 29
ID ABU91733 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 30
ID ABU89426 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 31
ID ABU86267 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 32
ID ABU67480 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 33
ID ABU80508 standard; protein; 678 AA.
DE Human PRO protein #75.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 34
ID ABU72488 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 35
ID ABU90892 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 36
ID ABO33951 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
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PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 37
ID ABR99426 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 38
ID ABR98816 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 39
ID ABO16339 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 40
ID ABR92239 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 41
ID ABO18880 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 42
ID ABR78301 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 43
ID ABR71968 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 44
ID ABR85037 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 45
ID ABO00176 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 46
ID ABO11508 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.

PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 47
ID ABO02153 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 48
ID ABR8727 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 49
ID ABR83422 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 50
ID ABO06223 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 51
ID ABR59259 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 52
ID ABO09321 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 53
ID ABO19185 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 54
ID ABO11203 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 55
ID ABR66821 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 56
ID ABO16034 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040060-A1.
PD 27-FEB-2003.

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Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 57
ID ABO13740 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 58
ID ABU71522 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 59
ID ABU65643 standard; protein; 678 AA.
DE Human secreted/transmembrane protein, SEQ ID 150.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 60
ID ABO07491 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 61
ID ABO03678 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 62
ID ABR67126 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 63
ID ABO15729 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 64
ID ABU56010 standard; protein; 678 AA.
DE Human secreted/transmembrane protein, PRO1277.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 65
ID ABU72303 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 66
ID ABU6538 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032102-A1.
PD 13-FEB-2003.

Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 67
ID ABU95283 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 68
ID ABU71186 standard; protein; 678 AA.
DE Human PRO1277 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 69
ID ABO07796 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 70
ID ABR70037 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 71
ID ABR69370 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 72
ID ABO01511 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 73
ID ABU81313 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 74
ID ABR60110 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 75
ID ABU90976 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 76
ID ABR67845 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027269-A1.
PD 06-FEB-2003.
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Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 77
ID ABR65233 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 78
ID ABR6455 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 79
ID ABR71867 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 80
ID ABUS9237 standard; protein; 678 AA.
DE Human secreted/transmembrane protein; #69.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 81
ID ABUS5347 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 82
ID ABUS9037 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 83
ID ABUS3117 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 84
ID ABUS9473 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 85
ID ABUS9521 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 86
ID ABUS4032 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 87
ID ABUS93683 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 88
ID ABUS934 standard; protein; 678 AA.
DE Human PRO1277 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 89
ID ABR64928 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 90
ID ABUS27297 standard; protein; 678 AA.
DE Human secreted/transmembrane polypeptide PRO1277.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 91
ID ABR68760 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003022271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 92
ID ABUS6576 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 93
ID ABR99121 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 94
ID ABUS7005 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 95
ID ABUS957 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003023300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 96
ID ABUS8244 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 97
ID ABU87255 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 98
ID ABU83727 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 99
ID ABO08101 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 100
ID ABU92492 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 101
ID ABU81812 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 102
ID ABU65976 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 103
ID ABU81162 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 104
ID ABU59805 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 105
ID ABU93993 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 106
ID ABU99846 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 107

ID ABR66516 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 108
ID ABR90934 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 109
ID ABO53277 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 110
ID ABU58943 standard; protein; 678 AA.
DE Human secreted/transmembrane protein, #69.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 111
ID ABU94361 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 112
ID ABU79243 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 113
ID ABU86572 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 114
ID ABU86817 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 115
ID ABU94666 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 116
ID ABO04593 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 117

ID ABR70342 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 118
ID ABU92321 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 119
ID ABU98507 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 120
ID ABR65906 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 120
ID ABR65906 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 121
ID ABR64623 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 122
ID ABU59386 standard; protein; 678 AA.
DE Novel human secreted or transmembrane protein PRO1135.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 123
ID ABU79548 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 124
ID ABU92939 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 125
ID ABU95898 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 126
ID ABU9118 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 127
ID ABU90211 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.

PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 128
ID AB009626 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 129
ID AB010898 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 130
ID ABR70952 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 131
ID ABU98279 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 131
ID ABU98279 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 132
ID ABU87560 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 133
ID ABU91428 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 134
ID ABU89284 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US200303634-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 135
ID ABU84642 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 136
ID ABR69732 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 137
ID ABU80109 standard; protein; 678 AA.
DE Human PRO protein #75.
PN US2003036139-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 138
ID ABU82491 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 139
ID ABU92152 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 140
ID ABU93378 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003017541-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 141
ID ABO09931 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003017543-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 142
ID ABO09016 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036152-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 143
ID ABU96455 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 144
ID ABU10658 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 145
ID ABU10584 standard; protein; 678 AA.
DE Human secreted/transmembrane protein #75.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 146
ID ABU81610 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002171164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 147
ID ABU72125 standard; protein; 678 AA.

DE Human PRO polypeptide #17.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 148
ID ABU95593 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 149
ID ABU96802 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 150
ID ABR70647 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 151
ID ABO04998 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 152
ID ABO08406 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 153
ID ABU88549 standard; protein; 678 AA.
DE Human secreted and transmembrane polypeptide PRO1277.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 154
ID ABO34063 standard; protein; 678 AA.
DE Human PRO1277 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 155
ID ABO05613 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 156
ID ABR74002 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 157

ID ABR95594 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US200305445-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 158
ID ABR80891 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 159
ID ABR81196 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 160
ID ABR00892 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 161
ID ABR88494 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 162
ID ABR77315 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 163
ID ABR028799 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 164
ID ABO31544 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 165
ID ABR07961 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 166
ID ABO40441 standard; protein; 678 AA.

DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 167
ID ABO35866 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 168
ID ABO44005 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 169
ID ADA77902 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 170
ID ABR24800 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 171
ID ABO03068 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 172
ID ABR90324 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 173
ID ABR17238 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 174
ID ABR94984 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 175
ID ABR95289 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 176
ID ADB17091 standard; protein; 678 AA.
DE Human transmembrane PRO polypeptide (Segid 34).
PD US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 177
ID ABO21527 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PD US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 178
ID ABR97791 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 179
ID ABR87579 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 180
ID ABR77620 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 181
ID ABM27850 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 182
ID ABM06131 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 183
ID ABM03637 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 184
ID ABM3508 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 185

ID ABM26325 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 186
ID ABO48107 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PD US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 187
ID ABR92849 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 188
ID ABO24610 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PD US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 189
ID ADA37690 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PD US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 190
ID ABM11621 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 191
ID ABM02722 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 192
ID ABM16018 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PD US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 193
ID ABO27579 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PD US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 194
ID ABM29070 standard; protein; 678 AA.

DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 195
ID ABM07046 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 196
ID ABM21140 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 197
ID ABM09486 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 198
ID ABO41356 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 199
ID ABO36171 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 200
ID ABO43700 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 201
ID ABM76400 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 202
ID ABM76096 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 203
ID ABM25715 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104542-A1.

PD 05-JUN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 204
ID ABM26020 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 205
ID ADA21376 standard; protein; 678 AA.
DE Human secreted/transmembrane polypeptide PRO1277.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 206
ID ABO03373 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 207
ID ABO02458 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 208
ID ABO44255 standard; protein; 678 AA.
DE Human secreted/transmembrane polypeptide PRO 1277.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 209
ID ABR90629 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 210
ID ABR73697 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 211
ID ABO16949 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 212
ID ABR94374 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 213
ID ABR75881 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044929-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 214
ID ABR71257 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 215
ID ABR93154 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 216
ID ABR93459 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 217
ID ADL10163 standard; protein; 678 AA.
DE Human secreted/transmembrane protein, PRO1277.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 218
ID ABR87884 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 219
ID ABO27884 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 220
ID ABO30019 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 221
ID ABO33228 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 222
ID ABO04916 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 223
ID ABO08876 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 224
ID ABO36476 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 225
ID ABO35561 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 226
ID ABO39526 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 227
ID ABO10401 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 228
ID ABO11926 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 229
ID ABO52072 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 230
ID ABO52377 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 231
ID ADL19696 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 232
ID ABO23695 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 233
ID ADB17279 standard; protein; 678 AA.
DE Human transmembrane PRO polypeptide (SeqID 34).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 234
ID ADA17707 standard; protein; 678 AA.
DE Human PRO1277 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 235
ID ABR97181 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 236
ID ABR86969 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 237
ID ABM11011 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 238
ID ABM28155 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 239
ID ABO32154 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 240
ID ABM15281 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 241
ID ABO06436 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 242
ID ABO04247 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 243
ID ABO22360 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 244
ID ABO07656 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 245
ID ABO40746 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 246
ID ABO35393 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 247
ID ABO33156 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 248
ID ABO52682 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 249
ID ABO50242 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
Pred. No. 1.1e-306;
RESULT 250
ID ABO99236 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040055-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 251
ID ABO04288 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 252
ID ABO05918 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 253
ID ABO18458 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 254
ID ADA27815 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 255
ID ABR97486 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 256
ID ABR80586 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 257
ID ABR01197 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 258
ID ABR88799 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 259
ID ABR113451 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 260
ID ABR20835 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 261
ID ABO41966 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 262
ID ABO42576 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003048751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 263
ID ABR10096 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 264
ID ABO38611 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 265
ID ABR32851 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 266
ID ABR22665 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 267
ID ABR74876 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 268
ID ABR79694 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 269
ID ABR96266 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 270
 ID ABO2417 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003059886-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 271
 ID ABR86359 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003049758-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 272
 ID ABR86664 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 273
 ID ABR16628 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003064448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 274
 ID ABR29680 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003064456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 275
 ID ABO29104 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 276
 ID ABR23885 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003068735-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 277
 ID ABR23275 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003068753-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 278
 ID ABR22055 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003068742-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 279
 ID ABO22137 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

ID ABO37696 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 280
 ID ABR28460 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003082715-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 281
 ID ABR28765 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003082716-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 282
 ID ABR66409 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003068737-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 283
 ID ABR75791 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003104547-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 284
 ID ABR34071 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003096359-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 285
 ID ABR34376 standard; protein; 678 AA.
 DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
 PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 286
 ID ABO20307 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 287
 ID ABO21222 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 6; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 288
 ID ABO22137 standard; protein; 678 AA.
 DE Human secreted/transmembrane protein (PRO) #75.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 289
ID ADA20068 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 290
ID ABO34183 standard; protein: 678 AA.
DE Human secreted/transmembrane polypeptide PRO 1277.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 291
ID ABR96571 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 292
ID ADA94395 standard; protein: 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 293
ID ABR85749 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 294
ID ABR9731 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 295
ID ABR00587 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 296
ID ABR00282 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 297
ID ABO29714 standard; protein: 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 298
ID ABR23580 standard; protein: 678 AA.

DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 299
ID ABR29375 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 300
ID ABO38306 standard; protein: 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 301
ID ABO45606 standard; protein: 678 AA.
DE Human PRO polypeptide #75.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 302
ID ABR20530 standard; protein: 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 303
ID ADA81421 standard; protein: 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 304
ID ABO16644 standard; protein: 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 305
ID ABO18270 standard; protein: 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 306
ID ABO22697 standard; protein: 678 AA.
DE Human PRO polypeptide #75.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 307
ID ABO23002 standard; protein: 678 AA.
DE Human PRO polypeptide #75.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 308
ID ABR92544 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 309
ID ABR81501 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 310
ID ABW77925 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 311
ID ABR89714 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 312
ID ABW26630 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 313
ID ABW13756 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 314
ID ABO28494 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 315
ID ABO30324 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 316
ID ABW07351 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 317

ID ABO03942 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 318
ID ABO37086 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 319
ID ABO41661 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 320
ID ABO35256 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 321
ID ABW25105 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 322
ID ABO47497 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003048742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 323
ID ABO47802 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 324
ID ABO48412 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 325
ID ABO51462 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003048766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 326
ID ABO51767 standard; protein; 678 AA.
DE Human PRO polypeptide #75.

PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 327
ID ABO50547 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 328
ID ABR79671 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 329
ID ABM16933 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 330
ID ABO17965 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 331
ID ABO20917 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 332
ID ABR96876 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 333
ID ADA38620 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003058780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 334
ID ABM12231 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 335
ID ABM16323 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 336
ID ABM24190 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 337
ID ABM14671 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 338
ID ABM04552 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 339
ID ABM06741 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 340
ID ABM09181 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 341
ID ABO39221 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 342
ID ABM75486 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 343
ID ABM25410 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 344
ID ABM19920 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 345
ID ABO46826 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 346
ID ABO47131 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 347
ID ADA83219 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 348
ID ABR71562 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 349
ID ABR72172 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 350
ID ABR98511 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 351
ID ABO06881 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 352
ID ABR84834 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 353
ID ABR73392 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 354
ID ABR76486 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 355
ID ABR73087 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 356
ID ABR18153 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 357
ID ABO20612 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 358
ID ABO25355 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 359
ID ABO25660 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 360
ID ABR94069 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 361
ID ADA92741 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 362
ID ABR79976 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 363
ID ABR11316 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 364
ID ABO32923 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 365
ID ABO30629 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 366
ID ABO30934 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 367
ID ABO27240 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 368
ID ABO29985 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 369
ID ABO05521 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 370
ID ABO15586 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 371
ID ABO08571 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 372
ID ABO42271 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003048748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 373
ID ABO38001 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 374

ID ABO45911 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 375
ID ABO66714 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 376
ID ABO20262 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 377
ID ABO19615 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 378
ID ABO49327 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 379
ID ABO49632 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 380
ID ADA78514 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 381
ID ABO88189 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 382
ID ADA00365 standard; protein; 678 AA.
DE Human secreted/transmembrane polypeptide PRO 1277.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 383
ID ABO26935 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
RESULT 384
ID ABM03332 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
RESULT 385
ID ABO39831 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;
RESULT 386
ID ABO49937 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 387
ID ABO50852 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 388
ID ABO5308 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 389
ID ABR74612 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 390
ID ABR77091 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 391
ID ABM17848 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 392
ID ABR35899 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 393

ID ABO21832 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 394
ID ABO20002 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 395
ID ABO24305 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 396
ID ABR86054 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 397
ID ABM10706 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 398
ID ABR76705 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 399
ID ABR89409 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 400
ID ABM12536 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073176-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 401
ID ABM05826 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 402
ID ABO34951 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 403
ID ABM03027 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 404
ID ABM19005 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 405
ID ABM19310 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 406
ID ABO46521 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 407
ID ABO49022 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 408
ID ABR69065 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 409
ID ABR89104 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 410
ID ABR72477 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 411
ID ABR74307 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 412
ID ABO18575 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 413
ID ABR80281 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 414
ID ABM01502 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 415
ID ABM02112 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 416
ID ABR87274 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 417
ID ABM12841 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 418
ID ABM30595 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 419
ID ABM24495 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 420
ID ABO29409 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 421
ID ABO31239 standard; protein; 678 AA.

DE Human secreted/transmembrane protein (PRO) #75.
FN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 422
ID ABM14366 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 423
ID ABM09791 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 424
ID ABO38916 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
FN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 425
ID ABM34681 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US200304538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 426
ID ABO51157 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
FN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 427
ID ABO03983 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
FN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 428
ID ABO10453 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
FN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 429
ID ABO53149 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
FN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 430
ID ABR77696 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 431
ID ABR78906 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 432
ID ABO24000 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
FN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 433
ID ABR93764 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 434
ID ABO1807 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 435
ID ABW78230 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003048764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 436
ID ABR90019 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 437
ID ADA22302 standard; protein; 678 AA.
DE Human secreted/transmembrane polypeptide PRO1277.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 438
ID ABM27545 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 439
ID ABM13146 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
FN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 440
ID ABO31849 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.

PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 441
ID AAM14061 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 442
ID AAM08266 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 443
ID ABO40136 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 444
ID ABM74571 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 445
ID ABM33766 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 446
ID AAM20225 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 447
ID ABO48717 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 448
ID ABO22519 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 449
ID ABR72782 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 450
ID ABO15424 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 451
ID ABR85139 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 452
ID ABO15119 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 453
ID ABO17254 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 454
ID ABO17543 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 455
ID ABO6468 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 456
ID ADA39161 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 457
ID ABR85444 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 458
ID ABM77010 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 459
ID ABO28189 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 460
ID ABM22970 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 461
ID ABM30290 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 462
ID ABM21750 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 463
ID ABM21445 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 464
ID ABM14976 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 465
ID ABM41051 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 466
ID ABO36781 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 467
ID ABO37391 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 468
ID ABM75181 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 469
ID ABM33461 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 470
ID ABO46216 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 471
ID ADA82585 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 472
ID ADB96187 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 473
ID ABM31815 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 474
ID ABM31205 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 475
ID ADB83693 standard; protein; 678 AA.
DE Human secreted/transmembrane protein (PRO) #75.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 476
ID ABM32120 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 477
ID ABM32425 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 478
ID ADB68286 standard; protein; 678 AA.
DE Human PRO1277 protein.

PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 479
ID ADB68093 standard; protein; 678 AA.
DE Human PRO1277 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 480
ID ADB31510 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 481
ID ADB30900 standard; protein; 678 AA.
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 482
ID ADB90910 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 483
ID ADC57659 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 484
ID ADC55023 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 485
ID ADC11890 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 486
ID ADC06990 standard; protein; 678 AA.
DE Human PRO1277 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 487
ID ADC56312 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;

RESULT 488
ID ADC17169 standard; protein; 678 AA.
DE Mammalian PRO polypeptide (SeqID 34).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 489
ID ADC07367 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 490
ID ADC11357 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 491
ID ADC14867 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 492
ID ADC52362 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 493
ID ADC14479 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 494
ID ADD06011 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 495
ID ADC81836 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 496
ID ADD07478 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;
RESULT 497
ID ADC82369 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;

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Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 498
ID ADD05623 standard; protein: 678 AA.
DE Human secreted/transmembrane.protein (PRO) #75.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 499
ID ADD08549 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 500
ID ADD06798 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 501
ID ADC83045 standard; protein: 678 AA.
DE Human PRO polypeptide #44.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 502
ID ADD55152 standard; protein: 678 AA.
DE Human PRO polypeptide #44.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 503
ID ADP36038 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 504
ID ADD56110 standard; protein: 678 AA.
DE Human PRO polypeptide #44.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 505
ID ADD54548 standard; protein: 678 AA.
DE Human PRO polypeptide #44.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 506
ID ADE26702 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 507
ID ADE26169 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 508
ID ADE67106 standard; protein: 678 AA.
DE Human PRO1277 amino acid sequence SEQ ID NO:179.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 509
ID ADG01039 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 510
ID ADG08592 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 511
ID ADG02618 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 512
ID ADG01325 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 513
ID ADF95500 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 514
ID ADF95313 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 515
ID ADG13315 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 516
ID ADH24066 standard; protein: 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

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RESULT 517
ID ADH34092 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 518
ID ADH29925 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 519
ID ADH23896 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 520
ID ADH08975 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 521
ID ADG85300 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 522
ID ADH24576 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 523
ID ADH37432 standard; protein; 678 AA.
DE Human secreted and transmembrane protein PRO1277.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 524
ID ADH02021 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 525
ID ADH37602 standard; protein; 678 AA.
DE Human secreted and transmembrane protein PRO1277.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 526
ID ADH53511 standard; protein; 678 AA.

ID ADG85640 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 527
ID ADH24236 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 528
ID ADH38530 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 529
ID ADG83651 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 530
ID ADH29459 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 531
ID ADH27575 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 532
ID ADH37772 standard; protein; 678 AA.
DE Human secreted and transmembrane protein PRO1277.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 533
ID ADH37949 standard; protein; 678 AA.
DE Human secreted and transmembrane protein PRO1277.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 534
ID ADH57369 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 535
ID ADH53511 standard; protein; 678 AA.

DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181636-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 536
 ID ADH93681 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181641-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 537
 ID ADH82017 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181638-A1.
 PD 25-SEP-2003
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 538
 ID ADH49872 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181639-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 539
 ID ADI25382 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181696-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 540
 ID ADH90175 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181698-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 541
 ID ADI25552 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181669-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 542
 ID ADH97726 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181672-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 543
 ID ADI35360 standard; protein; 678 AA.
 DE Human PRO polypeptide #44.
 PN US2003050457-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 544
 ID ADI03574 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181656-A1.
 PA (GETH) GENENTECH INC.

PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 545
 ID ADI11931 standard; protein; 678 AA.
 DE Human PRO polypeptide #17.
 PN US2003181686-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 546
 ID ADH90005 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181697-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 547
 ID ADH99852 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003049682-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 548
 ID ADH98406 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181707-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 549
 ID ADI11081 standard; protein; 678 AA.
 DE Human PRO polypeptide #17.
 PN US2003181682-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 550
 ID ADI11591 standard; protein; 678 AA.
 DE Human PRO polypeptide #17.
 PN US2003181684-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 551
 ID ADH98236 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181709-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 552
 ID ADH98576 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181708-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3502; DB 7; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 553
 ID ADH98066 standard; protein; 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003181673-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 554
ID AD105054 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 555
ID AD103404 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 556
ID AD104799 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 557
ID ADH78253 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 558
ID AD119597 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 559
ID ADH90345 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 560
ID AD103064 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 561
ID ADH77913 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 562
ID ADH97896 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
Query Match 100.0%; Score 3502; DB 7; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 563
ID AD101281 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 564
ID AD101976 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 565
ID AD103234 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 566
ID AD111421 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 567
ID AD102323 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 568
ID AD11761 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 569
ID AD105398 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 570
ID ADH79470 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 571
ID AD119427 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
Query Match 100.0%; Score 3502; DB 7; Length 678;

RESULT 572
ID ADI05228 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 573
ID ADH79640 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 574
ID ADI01466 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 575
ID ADI01636 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 576
ID ADI01606 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 577
ID ADH79810 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 578
ID ADI04628 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 579
ID ADI02764 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 580
ID ADH78083 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 581
ID ADH74287 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 582
ID ADI25892 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 583
ID ADK65404 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 584
ID ADH98746 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 585
ID ADH79987 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 586
ID ADL32756 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US200307396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 587
ID ADM30290 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 588
ID ADL93718 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 589
ID ADC52172 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 590
ID ADE74287 standard; protein; 678 AA.

[illegible]

Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 600		
ID ADH27745 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180912-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 601		
ID ADH25066 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180913-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 602		
ID ADH33718 standard; protein; 678 AA.		
DE Human PRO polypeptide #17.		
PN US2003181645-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 603		
ID ADG82799 standard; protein; 678 AA.		
DE Human PRO polypeptide #75.		
PN US2003215910-A1.		
PD 20-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 604		
ID ADH02361 standard; protein; 678 AA.		
DE Human PRO polypeptide #17.		
PN US2003180839-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 605		
ID ADH07968 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180845-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 606		
ID ADG69365 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180846-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 607		
ID ADH39186 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180917-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 608		
ID ADH26080 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003068770-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;
RESULT 609		
ID ADH26080 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003068770-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No.1,1e-306;

RESULT 609
ID ADG83926 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 610
ID ADH19425 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 611
ID ADG85470 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 612
ID ADH06264 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 613
ID ADH30094 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 614
ID ADH24406 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 615
ID ADH33049 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 616
ID ADG69535 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 617
ID ADH07798 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 618

ID ADG85810 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 619
ID ADH39356 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180816-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 620
ID ADH33548 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 621
ID ADH33888 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 622
ID ADH01098 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 623
ID ADG69705 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 624
ID ADH20918 standard; protein; 678 AA.
DE Human secreted/transmembrane protein PRO1277.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 625
ID ADH02191 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 626
ID ADG69195 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 627
ID ADG8580 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.

PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 628
ID ADH24916 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 629
ID ADH39533 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 630
ID ADH19958 standard; protein; 678 AA.
DE Human secreted/cransmembrane protein PRO1277.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 631
ID ADH02531 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 632
ID ADG69025 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 633
ID ADH07628 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 634
ID ADH86150 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 635
ID ADH24746 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 636
ID ADH25794 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180911-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 637
ID ADH38360 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 638
ID ADH57199 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 639
ID ADH52187 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 640
ID ADH49553 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 641
ID ADH90515 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 642
ID ADH11251 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 643
ID ADH98916 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 644
ID ADH02146 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 645
ID ADH90685 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181701-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 646
ID ADJ54788 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 647
ID ADJ98560 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 648
ID ADJ98730 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 649
ID ADJ78889 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187103-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 650
ID ADJ99123 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 651
ID ADJ99293 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 652
ID ADJ98911 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 653
ID ADJ79059 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 654
ID ADK00919 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 655
ID ADK14440 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 656
ID ADJ64559 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 657
ID ADM31455 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 658
ID ADM36502 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 659
ID ADM40307 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 660
ID ADM80889 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 661
ID ADM37915 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 662
ID ADJ77729 standard; protein; 678 AA.
DE Neoplastic disease detection protein PRO1277.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (BATO/) BATON D L.
PA (RIVV/) FILVAROFF E.
PA (GERR/) GERRITSEN W E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) MATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;
 RESULT 663
 ID AEA38448 standard; protein: 678 AA.
 DE Human secreted/cranmembrane protein, #112.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3502; DB 9; Length 678;
 RESULT 664
 ID AED50145 standard; protein: 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2005163766-A1.
 PD 28-JUL-2005.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3502; DB 9; Length 678;
 RESULT 665
 ID AEF12560 standard; protein: 678 AA.
 DE Human PRO1277 protein SEQ ID NO:34.
 PN US200608901-A1.
 PD 12-JAN-2006.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3502; DB 10; Length 678;
 RESULT 666
 ID AEF74249 standard; protein: 678 AA.
 DE Human PRO1277 protein SEQ ID NO:34.
 PN US2005260647-A1.
 PD 24-NOV-2005.
 PA (EATO/) EATON D L.
 PA (FILV/) FILVAROFF E.
 PA (GERR/) GERRITSEN M E.
 PA (GODO/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W L.
 Query Match
 Best Local Similarity 100.0%; Score 3502; DB 10; Length 678;
 RESULT 667
 ID ADB85607 standard; protein: 678 AA.
 DE Novel human secreted and transmembrane protein PRO1277.
 PN US2003049735-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 99.9%; Score 3493; DB 7; Length 678;
 RESULT 668
 ID ADJ70701 standard; protein: 693 AA.
 DE Human heat mitochondrial protein as a therapeutic target SegID2507.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 97.8%; Pred. No. 4.5e-305;
 RESULT 669
 ID AAB08815 standard; protein: 656 AA.
 DE Amino acid sequence of a human vitrin polypeptide.
 PN CA2235477-A1.
 PD 11-JUN-2000.
 PA (UABR-) UAB RES FOUND.
 Query Match
 Best Local Similarity 96.0%; Score 3344; DB 3; Length 656;
 RESULT 670
 ID ABG73355 standard; protein: 656 AA.
 DE Human ocular vitreous protein (vitrin).
 PN US2002160937-A1.
 PD 31-OCT-2002.
 PA (MAYN/) MAYNE R.
 PA (RENZ/) REN Z.
 PA (LIU/) LIU J.

Query Match
 Best Local Similarity 95.5%; Score 3344; DB 6; Length 656;
 RESULT 671
 ID AAB84763 standard; protein: 614 AA.
 DE Human diagnostic and therapeutic protein SEQ ID NO:5012.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 89.5%; Score 3136; DB 8; Length 614;
 RESULT 672
 ID ABB97508 standard; protein: 509 AA.
 DE Novel human protein SEQ ID NO: 776.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 72.4%; Score 2534.5; DB 5; Length 509;
 RESULT 673
 ID AAB85100 standard; protein: 329 AA.
 DE Human Zvwf1 polypeptide.
 PN WO200142466-A2.
 PD 14-JUN-2001.
 PA (ZYMO-) ZYMOGENETICS INC.
 Query Match
 Best Local Similarity 48.4%; Score 1695; DB 4; Length 329;
 RESULT 674
 ID AAO14430 standard; protein: 329 AA.
 DE Human von Willebrand factor type A domain superfamily member, Zvwf1.
 PN US2002004228-A1.
 PD 10-JAN-2002.
 PA (HOLL/) HOLLOWAY J L.
 Query Match
 Best Local Similarity 48.4%; Score 1695; DB 5; Length 329;
 RESULT 675
 ID ADF67846 standard; protein: 329 AA.
 DE Human Zvwf1.
 PN US2003077751-A1.
 PD 24-APR-2003.
 PA (HOLL/) HOLLOWAY J L.
 Query Match
 Best Local Similarity 99.7%; Pred. No. 7.6e-144;
 RESULT 676
 ID ADP29321 standard; protein: 531 AA.
 DE Human secreted protein SEQ ID #1319.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match
 Best Local Similarity 32.3%; Score 1130.5; DB 8; Length 531;
 RESULT 677
 ID AAY13383 standard; protein: 550 AA.
 DE Amino acid sequence of protein PRO294.
 PN WO9914328-A2.
 PD 25-MAR-1999.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 32.3%; Score 1129.5; DB 2; Length 550;
 RESULT 678
 ID AAY84405 standard; protein: 550 AA.
 DE Amino acid sequence of human COCH5B2 polypeptide.
 PN WO200018211-A2.
 PD 06-APR-2000.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match
 Best Local Similarity 32.3%; Score 1129.5; DB 3; Length 550;
 RESULT 679
 ID AAB80251 standard; protein: 550 AA.
 DE Human PRO294 protein.
 PN WO200104311-A1.
 PD 18-JAN-2001.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 32.3%; Score 1129.5; DB 4; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 680
ID AAB50429 standard; protein; 550 AA.
DE Human COCHSB2 protein.
PN WO200071081-A2.
PD 30-NOV-2000.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 32.3%; Score 1129.5; DB 4; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 681
ID AAU29046 standard; protein; 550 AA.
DE Human PRO polypeptide sequence #23.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 4; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 682
ID AAB58422 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 683
ID ABU71629 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 684
ID ABU87970 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 685
ID ABU84285 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 686
ID ABR66159 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 687
ID ABR65549 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 688
ID ABU99489 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 689
ID ABU82728 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 690
ID ABU98949 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 691
ID ABU71484 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 692
ID ABR68098 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 693
ID ABU96151 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 694
ID ABU92582 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 695
ID ABO08659 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 696
ID ABO02711 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 697
ID ABR74865 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 698
ID ABR94627 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 699
ID ABU85600 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

RESULT 700
ID ABU98760 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 701
ID ABU97975 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 702
ID ABU91681 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 703
ID ABU71930 standard; protein; 550 AA.
DE Human secreted/transmembrane protein PRO294.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 704
ID ABU89374 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 705
ID ABU86215 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 706
ID ABU67428 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 707
ID ABU80456 standard; protein; 550 AA.
DE Human PRO protein #23.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 708
ID ABO01813 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 709
ID ABR9374 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040063-A1.
PD 27-FEB-2003.

Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 710
ID ABR98764 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 711
ID ABO16287 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 712
ID ABR92187 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 713
ID ABO18828 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 714
ID ABR78249 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 715
ID ABR84985 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 716
ID ABO00124 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 717
ID ABO11456 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 718
ID ABO02101 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 719
ID ABU54386 standard; protein; 550 AA.
DE Human secreted/transmembrane protein PRO294.
PN US2002133240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 720
 ID AB08675 standard; protein; 550 AA.
 DE Novel human secreted and transmembrane protein PRO294.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 721
 ID AB083370 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 722
 ID AB006171 standard; protein; 550 AA.
 DE Novel human secreted and transmembrane protein PRO294.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 723
 ID AB059207 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 724
 ID AB009269 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 725
 ID AB019133 standard; protein; 550 AA.
 DE Novel human secreted and transmembrane protein PRO294.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 726
 ID AB01151 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 727
 ID AB06769 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 728
 ID AB015982 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 729
 ID AB013688 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 730

ID AB047401 standard; protein; 550 AA.
 DE Human secreted/transmembrane polypeptide PRO294.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 731
 ID AB065591 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein, SEQ ID 46.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 732
 ID AB007439 standard; protein; 550 AA.
 DE Human PRO polypeptide #23.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 733
 ID AB003626 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 734
 ID AB067074 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003027266-A1.
 PD 06-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 735
 ID AB015677 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003054483-A1.
 PD 20-MAR-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 736
 ID AB059589 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein, PRO294.
 PN US2003022298-A1.
 PD 30-JAN-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 737
 ID AB065286 standard; protein; 550 AA.
 DE Human PRO polypeptide #23.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 738
 ID AB095231 standard; protein; 550 AA.
 DE Novel human secreted and transmembrane protein PRO294.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 739
 ID AB071134 standard; protein; 550 AA.
 DE Human PRO294 protein.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 740
 ID AB007744 standard; protein; 550 AA.

DE Human PRO polypeptide #23.
PN US200302130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 741
ID ABR69985 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 742
ID ABR69318 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 743
ID ABO01459 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 744
ID ABR61261 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 745
ID ABR60058 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 746
ID ABR67793 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 747
ID ABR65181 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 748
ID ABR68403 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 749
ID ABR71815 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 750
ID ABR65295 standard; protein; 550 AA.

DE Human PRO polypeptide #23.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 751
ID ABR68985 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 752
ID ABR63065 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 753
ID ABR94921 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 754
ID ABR90469 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 755
ID ABR63980 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 756
ID ABR93631 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 757
ID ABR64876 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 758
ID ABR68708 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 759
ID ABO06524 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
Pred. No. 2.4e-92;
RESULT 760
ID ABR99069 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040068-A1.

PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 761
ID ABUS6953 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 762
ID ABUS64538 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #42.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 763
ID ABUS5905 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 764
ID ABUS67384 standard; protein; 550 AA.
DE Human secreted protein PRO294.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 765
ID ABUS82192 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 766
ID ABUS87203 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 767
ID ABUS83675 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 768
ID ABUS8049 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 769
ID ABUS14904 standard; protein; 550 AA.
DE Human secreted / transmembrane polypeptide PRO294.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 770
ID ABUS81760 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032104-A1.

PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 771
ID ABUS5924 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 772
ID ABUS9753 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 773
ID ABUS93941 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 774
ID ABUS9794 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 775
ID ABUS66464 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 776
ID ABUS90882 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 777
ID ABUS94309 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 778
ID ABUS79191 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 779
ID ABUS85520 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 780
ID ABUS86825 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 781
ID ABU94614 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 782
ID ABO04541 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 783
ID ABR70290 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 784
ID ABU98455 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 785
ID ABR65854 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GERTH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 786
ID ABR64571 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 787
ID ABU79496 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 788
ID ABU92887 standard; protein: 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 789
ID ABU95846 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 790
ID ABU91066 standard; protein: 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 791

ID ABU90159 standard; protein: 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 792
ID ABO09574 standard; protein: 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 793
ID ABO10846 standard; protein: 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 794
ID ABR70900 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 795
ID ABU87508 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 796
ID ABU91376 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 797
ID ABU84590 standard; protein: 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 798
ID ABR69680 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 799
ID ABU80057 standard; protein: 550 AA.
DE Human PRO protein #23.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 800
ID ABU69661 standard; protein: 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GERTH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 801
ID ABU93326 standard; protein: 550 AA.
DE Human PRO polypeptide #23.

PN US2003017541-A1.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 802
ID ABO09879 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 803
ID ABO08964 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 804
ID ABU10532 standard; protein: 550 AA.
DE Human secreted/transmembrane protein #23.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 805
ID ABU95541 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 806
ID ABU96750 standard; protein: 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 807
ID ABR70595 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 808
ID ABO04946 standard; protein: 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 809
ID ABO08354 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 810
ID ABO14843 standard; protein: 550 AA.
DE Human secreted / transmembrane polypeptide PRO294.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 811
ID ABO05561 standard; protein: 550 AA.

DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 812
ID ABR73950 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 813
ID ABR95542 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 814
ID ABR80839 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 815
ID ABR81144 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 816
ID ABR00840 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 817
ID ABR88442 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 818
ID ABR77263 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 819
ID ABO28747 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 820
ID ABO31492 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068725-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 821
ID AAM07909 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 822
ID ABO40389 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 823
ID ABO35814 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 824
ID ABO43953 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 825
ID AOA77798 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 826
ID AAM24748 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 827
ID ADB29432 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 828
ID ABO03016 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 829
ID ABR90272 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 830

ID ABM17186 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 831
ID ABR94932 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 832
ID ABR95237 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 833
ID ABO21475 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 834
ID ABR97739 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 835
ID ABR87527 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 836
ID ABM77568 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 837
ID ABM27798 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 838
ID ABM06079 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 839
ID ABM03585 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068722-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 840
ID ABM35036 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 841
ID ABM26273 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 842
ID ABO48055 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 843
ID ABR92797 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 844
ID ABO24558 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 845
ID ABM11569 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 846
ID ABM02670 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 847
ID ABM15966 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 848
ID ABO27527 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064451-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 849
ID ABM29018 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 850
ID ABM06994 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 851
ID ABM21088 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 852
ID ABM09434 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 853
ID ABO41304 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 854
ID ABO36119 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 855
ID ABO43648 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 856
ID ABM76348 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 857
ID ABM76044 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 858			
ID ABR25663 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003104542-A1.			
PD 05-JUN-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 859			
ID ABR25968 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003104543-A1.			
PD 05-JUN-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 860			
ID ABO03321 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003036127-A1.			
PD 20-FEB-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 861			
ID ABO02406 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003040061-A1.			
PD 27-FEB-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 862			
ID ABR90577 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003036130-A1.			
PD 20-FEB-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 863			
ID ABR3645 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003054468-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 864			
ID ABO16897 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003054470-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 865			
ID ABR94322 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003044917-A1.			
PD 06-MAR-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 866			
ID ABR75829 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003044929-A1.			
PD 06-MAR-2003.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 867			
ID ADA1828 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein, #44.			
PN US2003039971-A1.			
PD 27-FEB-2003			
PA (GETH) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	

Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 868			
ID ABO32795 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein PRO294.			
PN US2003045693-AA.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 869			
ID ABR71205 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003059880-AA.			
PD 27-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 870			
ID ABR93102 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003064465-AA.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 871			
ID ABR93407 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003054478-AA.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 872			
ID ABR87832 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068718-AA.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 873			
ID ABO27832 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003064454-AA.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 874			
ID ABO29967 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003064461-AA.			
PD 03-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 875			
ID ABO33176 standard; protein; 550 AA.			
DE Human PRO polypeptide #23.			
PN US2003068724-AA.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 876			
ID ABO4864 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068727-AA.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 877			
ID ABO4864 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068727-AA.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	32.3%	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%	Pred. No. 2.4e-92;	

RESULT 877
ID ABM08824 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 878
ID ABO36424 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 879
ID ABO35509 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 880
ID ABO39474 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 881
ID ABM10349 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 882
ID ABM1874 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 883
ID ABO52020 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 884
ID ABO52325 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 885
ID ABO23643 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 886
ID ABR97129 standard; protein; 550 AA.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 887
ID ABR86917 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 888
ID ABM10959 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003045782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 889
ID ABM28103 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 890
ID ABO32102 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 891
ID ABM15229 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 892
ID ABM06384 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 893
ID ABM04195 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 894
ID ABM22308 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 895
ID ABM07604 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.

PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 896
ID ABO40694 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 897
ID ABM35341 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 898
ID ABM33104 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 899
ID ABO52630 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 900
ID ABO50190 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 901
ID ABU99184 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 902
ID ABO04236 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 903
ID ABO05866 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 904
ID ABO34855 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

RESULT 905
ID ABM18406 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 906
ID ADA16263 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 907
ID ABR97434 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 908
ID ABR80534 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 909
ID ABM01145 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 910
ID ABR88747 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 911
ID ABM13399 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 912
ID ABM20783 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 913
ID ABO41914 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 914
ID ABO42524 standard; protein; 550 AA.

ID ABM28713 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 934
ID ABM66357 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068737-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 935
ID ABM75739 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104547-A1.
PD 05-JUN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 936
ID ABM34019 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096359-A1.
PD 22-MAY-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 937
ID ABM34324 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003100061-A1.
PD 29-MAY-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 938
ID ABO20255 standard; protein, 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 939
ID ABO21170 standard; protein, 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 940
ID ABO22085 standard; protein, 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054477-A1.
PD 20-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 941
ID ABR96519 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054460-A1.
PD 20-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 942
ID ABR85697 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049753-A1.
PD 13-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 943
ID ABR96679 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049763-A1.
PD 13-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 944
ID ABM00230 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 945
ID ABM00535 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 946
ID ABO29662 standard; protein, 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 947
ID ABM23528 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068736-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 948
ID ABM29323 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068679-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 949
ID ABO38254 standard; protein, 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068767-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 950
ID ABO45554 standard; protein, 550 AA.
DE Human PRO polypeptide #23.
PN US2003073182-A1.
PD 17-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 951
ID ABM20478 standard; protein, 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104557-A1.
PD 05-JUN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

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RESULT 952
ID ADA42408 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 953
ID ADA81317 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 954
ID ABO16592 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 955
ID ABO18218 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 956
ID ABO22645 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 957
ID ABO22950 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 958
ID ABR92492 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 959
ID ABR81449 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 960
ID ABO17533 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 961
ID ABM77873 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049783-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 962
ID ABR89662 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 963
ID ABM26578 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 964
ID ABM13704 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 965
ID ABO28442 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 966
ID ABO30272 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 967
ID ABM07299 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 968
ID ABM03890 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 969
ID ABO37034 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 970
ID ABO41609 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      32.3%; Score 1129.5; DB 6; Length 550;
  Best Local Similarity 37.1%; Pred. No. 2.4e-92;
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Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 971
ID ABO35204 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 972
ID ABM25053 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 973
ID ABO47445 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 974
ID ABO47750 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 975
ID ABO48360 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 976
ID ABO51410 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 977
ID ABO51715 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 978
ID ABO50495 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 979
ID ABR79619 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 980
ID ABM16881 standard; protein; 550 AA.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 981
ID ABO17913 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 982
ID ABO20865 standard; protein; 550 AA.
DE Human secreted/cranmembrane protein (PRO) #23.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 983
ID ABR96824 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 984
ID ABM12179 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 985
ID ABM16271 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 986
ID ABM24138 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 987
ID ABM14619 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 988
ID ABM04500 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 989
ID ABM06689 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 990
 ID AEM09129 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003073174-A1.
 PD 17-APR-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 991
 ID ABO39169 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003068775-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 992
 ID ABR75434 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003104545-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 993
 ID ABR25358 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003104541-A1.
 PD 05-JUN-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 994
 ID ABR19868 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003104554-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 995
 ID ABO46774 standard; protein; 550 AA.
 DE Human PRO polypeptide #23.
 PN US2003049762-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 996
 ID ABO47079 standard; protein; 550 AA.
 DE Human PRO polypeptide #23.
 PN US2003049765-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 997
 ID ADA83115 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003049752-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 998
 ID ABR71510 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003032133-A1.
 PD 13-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 999
 ID ABR72120 standard; protein; 550 AA.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003032136-A1.
 PD 13-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1000
 ID ABR98459 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003036129-A1.
 PD 20-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1001
 ID ABO06829 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003040053-A1.
 PD 27-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1002
 ID ABR84782 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003040057-A1.
 PD 27-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1003
 ID ABR73340 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003054467-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1004
 ID ABR76434 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003044932-A1.
 PD 06-MAR-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1005
 ID ABR73035 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003027270-A1.
 PD 06-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1006
 ID ABR18101 standard; protein; 550 AA.
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.
 PN US2003054469-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1007
 ID ABO20560 standard; protein; 550 AA.
 DE Human secreted/transmembrane protein (PRO) #23.
 PN US2003032126-A1.
 PD 13-FEB-2003.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1008
 ID ABO25303 standard; protein; 550 AA.
 DE Human PRO polypeptide #23.
 PN US2003054463-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1009
 ID ABO25608 standard; protein; 550 AA.

DE Human PRO polypeptide #23.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1010
ID ABR94017 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1011
ID ABR79924 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1012
ID ABR11264 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1013
ID ABO32871 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1014
ID ABO30577 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1015
ID ABO30882 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1016
ID ABR7188 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1017
ID ABR29933 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1018
ID ABR05469 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003045700-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1019
ID ABR15534 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1020
ID ABR08519 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1021
ID ABR042219 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1022
ID ABR037949 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1023
ID ABR045859 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1024
ID ABR66662 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1025
ID ABR20158 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1026
ID ABR19563 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1027
ID ABR049275 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1028
ID ABO49580 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1029
ID ADA78410 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1030
ID ABR88137 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1031
ID ABR26683 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1032
ID ABR03280 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 6; Length 550;
RESULT 1033
ID ABO39779 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1034
ID ABO49885 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1035
ID ABO50800 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1036
ID ABO05256 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1037
ID ABR74560 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1038
ID ABR77039 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1039
ID ADA16687 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1040
ID ABR17796 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1041
ID ABR95847 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1042
ID ADA13116 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1043
ID ABO21780 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1044
ID ABO19950 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1045
ID ABO24253 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 37.1%; Score 1129.5; DB 7; Length 550;
RESULT 1046
ID ABR86002 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.

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Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1047
ID AEM10654 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1048
ID ABM76653 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1049
ID ABR89357 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1050
ID ABM12484 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1051
ID ABM05774 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1052
ID ABO34899 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1053
ID ABM02975 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1054
ID ABM18953 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1055
ID ABM19258 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1056
ID ABR80229 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003048735-A1.
PD 13-MAR-2003.

RESULT 1056
ID ABO46469 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1057
ID ABO46970 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003048757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1058
ID ADA41984 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1059
ID ABR69013 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1060
ID ABR89052 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1061
ID ABR72425 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1062
ID ABR74255 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1063
ID ABO18523 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1064
ID ADA17331 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1065
ID ABR80229 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003048735-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1066
ID ABO01450 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1067
ID ABO2060 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1068
ID ABR87222 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1069
ID ABO12789 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1070
ID ABO30543 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1071
ID ABO24443 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1072
ID ABO29357 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1073
ID ABO31187 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1074
ID ABO14314 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1075
ID ABO09739 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1076
ID ABO38864 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1077
ID ABO34629 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1078
ID ABO51105 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1079
ID ADA42834 standard; protein: 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1080
ID ABO03931 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1081
ID ABO10401 standard; protein: 550 AA.
DE Human PRO polypeptide #23.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1082
ID ABR77644 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1083
ID ABR78854 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1084
ID ABO23948 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054482-A1.

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PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1085
ID ABR93712 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1086
ID ABM01755 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1087
ID ABM78178 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1088
ID ABR89967 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1089
ID ABM27493 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1090
ID ABM13094 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1091
ID ABO31797 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1092
ID ABM14009 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1093
ID ABM08214 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1094
ID ABO40084 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1095
ID ABM74519 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1096
ID ABM33714 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1097
ID ABM20173 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1098
ID ABO48665 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1099
ID ABR72730 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1100
ID ABO15372 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1101
ID ABR85087 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1102
ID ABO15067 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1103
ID ABO17202 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
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PN US2003040077-A1.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1104
ID ABM17491 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1105
ID ABR85392 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1106
ID ABO17594 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1107
ID ABW76958 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1108
ID ABO28137 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1109
ID ABM22918 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1110
ID ABM30238 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1111
ID AAM21698 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1112
ID AAM21393 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1113
ID ABM14924 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1114
ID ABO40999 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1115
ID ABO36729 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1116
ID ABO37339 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1117
ID ABW75129 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1118
ID ABM33409 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1119
ID ABO46164 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1120
ID ADA82481 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1121
ID ABM31763 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1122
ID AAM21393 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 1122
ID ADM31153 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1123
ID ADM7753 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1124
ID ADM7489 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1125
ID ADM85789 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1126
ID ADM32068 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1127
ID ADM32373 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1128
ID ADM31458 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1129
ID ADM30848 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1130
ID ADC28535 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1131

ID ADC39735 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1132
ID ADC40249 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1133
ID ADC19073 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1134
ID ADC34373 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1135
ID ADC29428 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1136
ID ADC28959 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1137
ID ADC40844 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1138
ID ADC19501 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1139
ID ADC33949 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1140
ID ADC13019 standard; protein; 550 AA.

DE Human secreted/transmembrane protein, #44.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1141
ID ADG12471 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1142
ID ADD05519 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1143
ID ADD05026 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1144
ID ADD04032 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1145
ID ADD03608 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1146
ID ADD34860 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1147
ID ADD02514 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1148
ID ADE01221 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1149
ID ADE95396 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.

PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1150
ID ADE12211 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1151
ID ADH08871 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1152
ID ADH59343 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1153
ID ADI38122 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1154
ID ADJ26390 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1155
ID ADI32652 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1156
ID ADM30186 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1157
ID ADE79305 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1158
ID ADE79729 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003130489-A1.
PD 10-JUL-2003.

PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1159
ID ADE73405 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1160
ID ADE74183 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1161
ID ADE73940 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1162
ID ADE74795 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1163
ID ADE99494 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1164
ID ADE98613 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1165
ID ADE99040 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1166
ID ADG40510 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US200325253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILT/) WILTAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1167
ID ADF73904 standard; protein; 550 AA.

DE Human secreted/transmembrane protein, #44.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1168
ID ADF96008 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003215903-A1.
PD 20-NOV-2003.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1169
ID ADF73480 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1170
ID ADG04279 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1171
ID ADG00439 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1172
ID ADG82695 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1173
ID ADG92232 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1174
ID ADG92750 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1175
ID ADH25976 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1176
ID ADH32945 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2003068768-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1177
ID ADH20539 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1178
ID ADH07394 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A. J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1179
ID ADH59939 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1180
ID ADH06567 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A. J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1181
ID ADI18709 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1182
ID ADI65429 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1183
ID ADI37688 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1184

ID ADH97488 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1185
ID ADI65856 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1186
ID ADH60599 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A. J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1187
ID ADI20064 standard; protein; 550 AA.
DE Protein #1 of the invention.
PN WO2004003020-A1.
PD 08-JAN-2004.
PA (NIME-) NIPPON MEDICAL SCHOOL FOUND.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1188
ID ADJ99656 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1189
ID ADI08849 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1190
ID ADJ54684 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1191
ID ADW25190 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1192
ID ADM29940 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003190611-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1193
ID ADJ64455 standard; protein; 550 AA.
DE Human PRO polypeptide #23.
PD US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1194
ID ADM31351 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PD US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1195
ID ADM36398 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PD US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1196
ID ADM40203 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PD US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1197
ID ADO06262 standard; protein; 550 AA.
DE Human PRO polypeptide #40.
PD US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1198
ID ADN37811 standard; protein; 550 AA.
DE Novel human secreted and transmembrane protein PRO294.
PD US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1199
ID ADR1114 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PD US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1200
ID ADR18023 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PD US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.

PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1201
ID ADS74662 standard; protein; 550 AA.
DE Human secreted/transmembrane protein #44.
PD US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1202
ID ADT03699 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PD US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1203
ID ADU06473 standard; protein; 550 AA.
DE Novel bronchial cancer-associated human protein SegID697.
PD DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 32.3%; Score 1129.5; DB 8; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1204
ID AEA37937 standard; protein; 550 AA.
DE Human secreted/transmembrane protein, #44.
PD US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 9; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1205
 ID AED23971 standard; protein; 550 AA.
 DE Human secreted protein PRO 294, SEQ ID 227.
 PN US2005214904-A1.
 PD 29-SEP-2005.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 9; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1206
 ID AED50041 standard; protein; 550 AA.
 DE Novel human secreted and transmembrane protein PRO294.
 PN US2005163766-A1.
 PD 28-JUN-2005.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 9; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1207
 ID AEB69140 standard; protein; 550 AA.
 DE Collagen homologous PRO294 protein, SEQ ID 227.
 PN US6974689-B1.
 PD 13-DEC-2005.
 PA (GETH) GENENTECH INC.
 Query Match 32.3%; Score 1129.5; DB 10; Length 550;
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;
 RESULT 1208
 ID AD041974 standard; protein; 615 AA.
 DE Human cell adhesion and extracellular matrix protein 3 SegID3.
 PN WO2004048529-A2.
 PD 10-JUN-2004.
 PA (INCYT-) INCYTE CORP.
 Query Match 32.2%; Score 1127.5; DB 8; Length 615;
 Best Local Similarity 37.1%; Pred. No. 4.3e-92;
 RESULT 1209
 ID ADC78547 standard; protein; 550 AA.
 DE Human PRO294 protein.
 PN WO20015796-A2.
 PD 23-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 32.2%; Score 1126.5; DB 3; Length 550;
 Best Local Similarity 37.1%; Pred. No. 4.4e-92;
 RESULT 1210
 ID AAB50430 standard; protein; 550 AA.
 DE Human mutant COCH5B2 protein.
 PN WO200071081-A2.
 PD 30-NOV-2000.
 PA (BCHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 32.0%; Score 1121.5; DB 4; Length 550;
 Best Local Similarity 36.9%; Pred. No. 1.3e-91;
 RESULT 1211
 ID AAY84406 standard; protein; 552 AA.
 DE Amino acid sequence of a murine COCH5B2 polypeptide.
 PN WO200018211-A2.
 PD 06-APR-2000.
 PA (BCHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 31.8%; Score 1113; DB 3; Length 552;
 Best Local Similarity 36.2%; Pred. No. 7.4e-91;
 RESULT 1212
 ID AEA90324 standard; protein; 432 AA.
 DE Human NOV12a SEQ ID NO 32.
 PN WO2003064629-A2.
 PD 07-AUG-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 27.7%; Score 969.5; DB 7; Length 432;
 Best Local Similarity 44.4%; Pred. No. 4.6e-76;
 RESULT 1213
 ID AAB08817 standard; protein; 178 AA.
 DE A von Willebrand A domain derived from a human vitrin polypeptide.
 PN CA2255477-A1.
 PD 11-JUN-2000.
 PA (UABR-) UAB RES FOUND.
 Query Match 26.1%; Score 915; DB 3; Length 178;
 Best Local Similarity 100.0%; Pred. No. 8.8e-74;

RESULT 1214
 ID ADR41420 standard; protein; 204 AA.
 DE Human CD-like molecule HACAD35, SEQ ID NO:219.
 PN WO200226930-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 25.8%; Score 904.5; DB 5; Length 204;
 Best Local Similarity 90.5%; Pred. No. 9.9e-73;
 RESULT 1215
 ID AAM17950 standard; protein; 172 AA.
 DE Peptide #4384 encoded by probe for measuring cervical gene expression.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.6%; Score 898; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.9e-72;
 RESULT 1216
 ID ABB36981 standard; peptide; 172 AA.
 DE Peptide #4487 encoded by human foetal liver single exon probe.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.6%; Score 898; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.9e-72;
 RESULT 1217
 ID AAM13577 standard; protein; 171 AA.
 DE Peptide #11 encoded by probe for measuring cervical gene expression.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1218
 ID ABB32505 standard; peptide; 171 AA.
 DE Peptide #11 encoded by human foetal liver single exon nucleic acid probe.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1219
 ID AAM23974 standard; protein; 171 AA.
 DE Peptide #11 encoded by probe for measuring placental gene expression.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1220
 ID ABB27360 standard; peptide; 171 AA.
 DE Human peptide #11 encoded by breast cell single exon nucleic acid probe.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1221
 ID ABB18012 standard; protein; 171 AA.
 DE Protein #11 encoded by probe for measuring heart cell gene expression.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1222
 ID AAM65717 standard; protein; 171 AA.
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26023.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 25.5%; Score 892; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;
 RESULT 1223

ID AAM53340 standard; protein; 171 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25445.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 25.5%; Score 892; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.9e-72;
RESULT 1224
ID ABG47358 standard; peptide; 171 AA.
DE Human liver peptide, SEQ ID NO 26006.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 25.5%; Score 892; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.9e-72;
RESULT 1225
ID AAM01329 standard; protein; 171 AA.
DE Peptide #11 encoded by probe for measuring human breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 25.5%; Score 892; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.9e-72;
RESULT 1226
ID ABG3347 standard; peptide; 171 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25012.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 25.5%; Score 892; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.9e-72;
RESULT 1227
ID AAU19651 standard; protein; 186 AA.
DE Human novel extracellular matrix protein, Seq ID NO 301.
PN W0200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.3%; Score 885; DB 4; Length 186;
Best Local Similarity 99.4%; Pred. No. 4.9e-71;
RESULT 1228
ID AAU87279 standard; protein; 186 AA.
DE Novel central nervous system protein #189.
PN W0200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.3%; Score 885; DB 4; Length 186;
Best Local Similarity 99.4%; Pred. No. 4.9e-71;
RESULT 1229
ID ABP47871 standard; protein; 186 AA.
DE Human polypeptide SEQ ID NO 301.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 25.3%; Score 885; DB 5; Length 186;
Best Local Similarity 99.4%; Pred. No. 4.9e-71;
RESULT 1230
ID ADC1083 standard; protein; 186 AA.
DE Human extracellular matrix protein from gene 26.
PN US200305875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.3%; Score 885; DB 7; Length 186;
Best Local Similarity 99.4%; Pred. No. 4.9e-71;
RESULT 1231
ID ADI34594 standard; protein; 186 AA.
DE Novel human protein seq id 797.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match 25.3%; Score 885; DB 8; Length 186;
Best Local Similarity 99.4%; Pred. No. 4.9e-71;
RESULT 1232
ID AAB08816 standard; protein; 160 AA.
DE A von Willebrand A domain derived from a human vitrin polypeptide.
PN CA225477-A1.
PD 11-JUN-2000.
PA (UABR-) UAB RES FOUND.
Query Match 22.8%; Score 799; DB 3; Length 160;
Best Local Similarity 98.8%; Pred. No. 2.3e-63;
RESULT 1233
ID ADU76366 standard; protein; 3067 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1618.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 15.8%; Score 552; DB 8; Length 3067;
Best Local Similarity 27.5%; Pred. No. 6.8e-39;
RESULT 1234
ID ABB90762 standard; protein; 3063 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 257.
PN W0200210217-A2.
PD 07-FEB-2002.
PA (UYUO-) UNIV JOHNS HOPKINS.
Query Match 15.5%; Score 543.5; DB 5; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4e-38;
RESULT 1235
ID ABU54469 standard; protein; 3063 AA.
DE Human tumour endothelial marker TEM 36.
PN W0200283874-A2.
PD 24-OCT-2002.
PA (UYUO-) UNIV JOHNS HOPKINS.
Query Match 15.5%; Score 543.5; DB 6; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4e-38;
RESULT 1236
ID ABR47415 standard; protein; 3063 AA.
DE Breast cancer associated protein sequence SEQ ID NO:61.
PN W02003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 15.5%; Score 543.5; DB 6; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4e-38;
RESULT 1237
ID AAU27790 standard; protein; 3118 AA.
DE Human full-length polypeptide sequence #115.
PN W0200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.5%; Score 543.5; DB 4; Length 3118;
Best Local Similarity 27.7%; Pred. No. 4.1e-38;
RESULT 1238
ID ABR47416 standard; protein; 3063 AA.
DE Breast cancer associated protein sequence SEQ ID NO:63.
PN W02003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 15.5%; Score 542.5; DB 6; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4.9e-38;
RESULT 1239
ID ADU75666 standard; protein; 3063 AA.
DE Marker gene related amino acid sequence SEQ ID NO:918.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 15.5%; Score 542.5; DB 8; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4.9e-38;
RESULT 1240
ID AAR57349 standard; protein; 496 AA.
DE Human cartilage matrix protein.
PN W09415627-A1.
PD 21-JUL-1994.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 14.3%; Score 501.5; DB 2; Length 496;

Best Local Similarity 28.8%; Pred. No. 1.2e-35;
 RESULT 1241
 ID ADP54237 standard; protein; 2000 AA.
 DE Human PRO protein sequence SEQ ID NO.213.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.5%; Score 471.5; DB 8; Length 2000;
 Best Local Similarity 30.9%; Pred. No. 6.3e-32;
 RESULT 1242
 ID ADY14520 standard; protein; 2000 AA.
 DE PRO polypeptide SEQ ID NO 326.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Query Match 13.5%; Score 471.5; DB 9; Length 2000;
 Best Local Similarity 30.9%; Pred. No. 6.3e-32;
 RESULT 1243
 ID ADQ39661 standard; protein; 2211 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1324.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 13.5%; Score 471.5; DB 8; Length 2211;
 Best Local Similarity 30.9%; Pred. No. 7.5e-32;
 RESULT 1244
 ID ADQ39658 standard; protein; 2244 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1321.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 13.5%; Score 471.5; DB 8; Length 2244;
 Best Local Similarity 30.9%; Pred. No. 7.7e-32;
 RESULT 1245
 ID ADQ39660 standard; protein; 2411 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1323.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 13.5%; Score 471.5; DB 8; Length 2411;
 Best Local Similarity 30.9%; Pred. No. 8.6e-32;
 RESULT 1246
 ID ABW8256 standard; protein; 2977 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO.2815.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 13.5%; Score 471.5; DB 8; Length 2977;
 Best Local Similarity 30.9%; Pred. No. 1.2e-31;
 RESULT 1247
 ID ADQ39657 standard; protein; 2977 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1320.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 13.5%; Score 471.5; DB 8; Length 2977;
 Best Local Similarity 30.9%; Pred. No. 1.2e-31;
 RESULT 1248
 ID ABR39571 standard; protein; 3151 AA.
 DE Human alpha3 collagen VI mature chain.
 PN WO2003015615-A2.
 PD 27-FEB-2003.
 PA (UYBR-) UNIV BROWN RES FOUND.
 Query Match 13.5%; Score 471.5; DB 6; Length 3151;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1249
 ID ABR90743 standard; protein; 3173 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 218.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 13.5%; Score 471.5; DB 5; Length 3173;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;

RESULT 1250
 ID ABUS4450 standard; protein; 3173 AA.
 DE Human tumour endothelial marker TEM 12.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 13.5%; Score 471.5; DB 6; Length 3173;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1251
 ID ABR39570 standard; protein; 3176 AA.
 DE Human alpha3 collagen VI precursor chain.
 PN WO2003015615-A2.
 PD 27-FEB-2003.
 PA (UYBR-) UNIV BROWN RES FOUND.
 Query Match 13.5%; Score 471.5; DB 6; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1252
 ID ADP6255 standard; protein; 3176 AA.
 DE Human alpha 3 type VI collagen, isoform 1 precursor.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 13.5%; Score 471.5; DB 7; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1253
 ID ADQ18247 standard; protein; 3176 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1065.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1254
 ID ADQ29665 standard; protein; 3176 AA.
 DE Human colorectal cancer-associated protein #20.
 PN EP143393-A2.
 PD 21-JUL-2004.
 PA (FARB) BAYER HEALTHCARE LLC.
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1255
 ID ADR87616 standard; protein; 3176 AA.
 DE Human type VI collagen alpha 3, SEQ ID 20.
 PN WO2004075835-A2.
 PD 10-SEP-2004.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1256
 ID ADU06731 standard; protein; 3176 AA.
 DE Novel bronchial cancer-associated human protein SegID957.
 PN DE10316701-A1.
 PD 04-NOV-2004.
 PA (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTRANOS-VELEZ E.
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1257
 ID ADV70236 standard; protein; 3176 AA.
 DE Tumor-associated antigenic target polypeptide TAT475.
 PN WO2004112829-A2.
 PD 29-DEC-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.5%; Score 471.5; DB 9; Length 3176;
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;
 RESULT 1258
 ID ADZ80431 standard; protein; 3176 AA.
 DE Mature collagen alpha 3 (VI) chain SEQ ID NO 44.
 PN WO2005040422-A2.
 PD 06-MAY-2005.
 PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 13.5%; Score 471.5; DB 9; Length 3176;
Best Local Similarity 30.9%; Pred. No. 1.4e-31;
RESULT 1259
ID AFB69977 standard; protein; 3176 AA.
DE Colorectal cancer-associated marker protein SEQ ID NO:155.
PN WO2006015047-A2.
PD 09-FEB-2006.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 13.5%; Score 471.5; DB 10; Length 3176;
Best Local Similarity 30.9%; Pred. No. 1.4e-31;
RESULT 1260
ID AAM40303 standard; protein; 3177 AA.
DE Human polypeptide SEQ ID NO 3448.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.5%; Score 471.5; DB 4; Length 3177;
Best Local Similarity 30.9%; Pred. No. 1.4e-31;
RESULT 1261
ID ADO39656 standard; protein; 3177 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1319.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 13.5%; Score 471.5; DB 8; Length 3177;
Best Local Similarity 30.9%; Pred. No. 1.4e-31;
RESULT 1262
ID ADZ12635 standard; protein; 499 AA.
DE Human cancer-associated protein #43.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 454; DB 9; Length 499;
Best Local Similarity 27.0%; Pred. No. 2.4e-31;
RESULT 1263
ID ADZ12643 standard; protein; 499 AA.
DE Human cancer-associated protein #47.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 454; DB 9; Length 499;
Best Local Similarity 27.0%; Pred. No. 2.4e-31;
RESULT 1264
ID AAM06236 standard; protein; 159 AA.
DE Peptide #4918 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 12.9%; Score 452.5; DB 4; Length 159;
Best Local Similarity 51.2%; Pred. No. 4.7e-32;
RESULT 1265
ID ADQ65418 standard; protein; 243 AA.
DE Novel human protein sequence #391.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.8%; Score 448.5; DB 8; Length 243;
Best Local Similarity 38.2%; Pred. No. 2.2e-31;
RESULT 1266
ID AAM93257 standard; protein; 540 AA.
DE Human polypeptide, SEQ ID NO: 2705.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.8%; Score 447.5; DB 4; Length 540;
Best Local Similarity 26.4%; Pred. No. 1e-30;
RESULT 1267
ID ADL30672 standard; protein; 540 AA.
DE Human protein encoded by a full length cDNA clone SegID 2705.
PN EPI1396543-A2.
PD 10-MAR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.8%; Score 447.5; DB 8; Length 540;
Best Local Similarity 26.4%; Pred. No. 1e-30;
RESULT 1268
ID ADZ12637 standard; protein; 540 AA.
DE Human cancer-associated protein #44.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 12.7%; Score 446.5; DB 9; Length 540;
Best Local Similarity 26.4%; Pred. No. 1.3e-30;
RESULT 1269
ID ADZ12641 standard; protein; 540 AA.
DE Human cancer-associated protein #46.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 12.7%; Score 446.5; DB 9; Length 540;
Best Local Similarity 26.4%; Pred. No. 1.3e-30;
RESULT 1270
ID ADO39655 standard; protein; 2210 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1318.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 446.5; DB 8; Length 2210;
Best Local Similarity 29.0%; Pred. No. 1.4e-29;
RESULT 1271
ID AAM93255 standard; protein; 558 AA.
DE Human polypeptide, SEQ ID NO: 2701.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.5%; Score 436; DB 4; Length 558;
Best Local Similarity 24.7%; Pred. No. 1.2e-29;
RESULT 1272
ID ADL30668 standard; protein; 558 AA.
DE Human protein encoded by a full length cDNA clone SegID 2701.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.5%; Score 436; DB 8; Length 558;
Best Local Similarity 24.7%; Pred. No. 1.2e-29;
RESULT 1273
ID ADO41980 standard; protein; 575 AA.
DE Human cell adhesion and extracellular matrix protein 9 SegID9.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.5%; Score 436; DB 8; Length 575;
Best Local Similarity 24.7%; Pred. No. 1.3e-29;
RESULT 1274
ID ADO41982 standard; protein; 534 AA.
DE Human cell adhesion and extracellular matrix protein 11 SegID11.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.4%; Score 435.5; DB 8; Length 534;
Best Local Similarity 25.9%; Pred. No. 1.2e-29;
RESULT 1275
ID ADQ19949 standard; protein; 580 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2769.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.4%; Score 434; DB 8; Length 580;
Best Local Similarity 24.7%; Pred. No. 1.9e-29;
RESULT 1276
ID ADR66966 standard; protein; 581 AA.
DE Human cancer associated protein sequence SEQ ID NO:12.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match	12.4%;	Score 434;	DB 8;	Length 581;
Best Local Similarity	24.7%;	Pred. No. 1.9e-29;		
RESULT 1277				
ID ADZ12645 standard; protein; 581 AA.				
DE Human cancer-associated protein #48.				
PN WO2005031001-A2.				
PD 07-APR-2005.				
PA (CHIR) CHIRON CORP.				
Query Match	12.4%;	Score 434;	DB 9;	Length 581;
Best Local Similarity	24.7%;	Pred. No. 1.9e-29;		
RESULT 1278				
ID ADZ12647 standard; protein; 581 AA.				
DE Human cancer-associated protein #49.				
PN WO2005031001-A2.				
PD 07-APR-2005.				
PA (CHIR) CHIRON CORP.				
Query Match	12.4%;	Score 434;	DB 9;	Length 581;
Best Local Similarity	24.7%;	Pred. No. 1.9e-29;		
RESULT 1279				
ID ADZ12649 standard; protein; 620 AA.				
DE Human cancer-associated protein #50.				
PN WO2005031001-A2.				
PD 07-APR-2005.				
PA (CHIR) CHIRON CORP.				
Query Match	12.3%;	Score 431.5;	DB 9;	Length 620;
Best Local Similarity	23.7%;	Pred. No. 3.7e-29;		
RESULT 1280				
ID ADQ39659 standard; protein; 2205 AA.				
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1322				
PN WO2004058052-A2.				
PD 15-JUL-2004.				
PA (APPL-) APPLERA CORP.				
Query Match	11.9%;	Score 416.5;	DB 8;	Length 2205;
Best Local Similarity	27.8%;	Pred. No. 7e-27;		
RESULT 1281				
ID ADQ39662 standard; protein; 2971 AA.				
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1325				
PN WO2004058052-A2.				
PD 15-JUL-2004.				
PA (APPL-) APPLERA CORP.				
Query Match	11.9%;	Score 416.5;	DB 8;	Length 2971;
Best Local Similarity	27.8%;	Pred. No. 1.1e-26;		
RESULT 1282				
ID ADR66963 standard; protein; 644 AA.				
DE Mouse cancer associated protein sequence SEQ ID NO.9.				
PN WO2004074321-A2.				
PD 02-SEP-2004.				
PA (SMGR-) SMGRES DISCOVERY INC.				
Query Match	11.8%;	Score 412.5;	DB 8;	Length 644;
Best Local Similarity	22.6%;	Pred. No. 2e-27;		
RESULT 1283				
ID ADZ12632 standard; protein; 644 AA.				
DE Murine cancer-associated protein #21.				
PN WO2005031001-A2.				
PD 07-APR-2005.				
PA (CHIR) CHIRON CORP.				
Query Match	11.8%;	Score 412.5;	DB 9;	Length 644;
Best Local Similarity	22.6%;	Pred. No. 2e-27;		
RESULT 1284				
ID ADB64658 standard; protein; 1036 AA.				
DE Human protein encoded by clone MESAN20027900.				
PN EPI308459-A2.				
PD 07-MAY-2003.				
PA (HELI-) HELIX RES INST.				
Query Match	11.8%;	Score 412;	DB 7;	Length 1036;
Best Local Similarity	29.3%;	Pred. No. 5e-27;		
RESULT 1285				
ID AAM93707 standard; protein; 488 AA.				
DE Human polypeptide, SEQ ID NO. 3641.				
PN EPI130094-A2.				
PD 05-SEP-2001.				
PA (HELI-) HELIX RES INST.				

Query Match	11.7%;	Score 409;	DB 4;	Length 488;
Best Local Similarity	26.0%;	Pred. No. 2.6e-27;		
RESULT 1286				
ID	ADJ1608 standard; protein; 488 AA.			
DE	Human protein encoded by a full length cDNA clone SegID 3641.			
PN	EP1396543-A2.			
PD	10-MAR-2004.			
PA	(REAS-) RRS ASSOC BIOTECHNOLOGY.			
Query Match	11.7%;	Score 409;	DB 8;	Length 488;
Best Local Similarity	26.0%;	Pred. No. 2.6e-27;		
RESULT 1287				
ID	AAM18620 standard; protein; 75 AA.			
DE	Peptide #5054 encoded by probe for measuring cervical gene expression.			
PN	WO200157278-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1288				
ID	AAM13573 standard; protein; 75 AA.			
DE	Peptide #7 encoded by probe for measuring cervical gene expression.			
PN	WO200157278-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1289				
ID	ABR32501 standard; peptide; 75 AA.			
DE	Peptide #7 encoded by human foetal liver single exon nucleic acid probe			
PN	WO200157277-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1290				
ID	ABR37861 standard; peptide; 75 AA.			
DE	Peptide #5367 encoded by human foetal liver single exon probe.			
PN	WO200157277-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1291				
ID	AAM25970 standard; protein; 75 AA.			
DE	Peptide #7 encoded by probe for measuring placental gene expression.			
PN	WO200157272-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1292				
ID	AAM13267 standard; protein; 75 AA.			
DE	Peptide #5304 encoded by probe for measuring placental gene expression.			
PN	WO200157272-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1293				
ID	ABR27356 standard; peptide; 75 AA.			
DE	Human peptide #7 encoded by breast cell single exon nucleic acid probe.			
PN	WO200157271-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1294				
ID	ABR18008 standard; protein; 75 AA.			
DE	Protein #7 encoded by probe for measuring heart cell gene expression.			
PN	WO200157274-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1295				
ID	ABR18008 standard; protein; 75 AA.			
DE	Protein #7 encoded by probe for measuring heart cell gene expression.			
PN	WO200157274-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1296				
ID	ABR18008 standard; protein; 75 AA.			
DE	Protein #7 encoded by probe for measuring heart cell gene expression.			
PN	WO200157274-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;	DB 4;	Length 75;
Best Local Similarity	100.0%;	Pred. No. 3.2e-26;		
RESULT 1297				
ID	ABR18008 standard; protein; 75 AA.			
DE	Protein #7 encoded by probe for measuring heart cell gene expression.			
PN	WO200157274-A2.			
PD	09-AUG-2001.			
PA	(MOLE-) MOLECULAR DYNAMICS INC.			
Query Match	10.9%;	Score 382;		

Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1295
ID ABB3120 standard; protein; 75 AA.
DE Protein #5119 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1296
ID AAM65713 standard; protein; 75 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26019.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1297
ID AAM70991 standard; protein; 75 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31297.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1298
ID AAM5336 standard; protein; 75 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25441.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1299
ID AAM58308 standard; protein; 75 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30413.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1300
ID ABG47354 standard; peptide; 75 AA.
DE Human liver peptide, SEQ ID No 26002.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1301
ID ABG52707 standard; peptide; 75 AA.
DE Human liver peptide, SEQ ID No 31355.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1302
ID AAM01325 standard; protein; 75 AA.
DE Peptide #7 encoded by probe for measuring human breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1303
ID ABG40779 standard; peptide; 75 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30444.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 5; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;

RESULT 1304
ID ABG35343 standard; peptide; 75 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25008.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.9%; Score 382; DB 5; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 1305
ID ABJ10550 standard; protein; 896 AA.
DE Human NOV4b protein.
PN W0200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.9%; Score 380; DB 5; Length 896;
Best Local Similarity 18.2%; Pred. No. 3.1e-24;
RESULT 1306
ID ADH17468 standard; protein; 896 AA.
DE Human NOV13g protein - SEQ ID 158.
PN W02003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.9%; Score 380; DB 8; Length 896;
Best Local Similarity 18.2%; Pred. No. 3.1e-24;
RESULT 1307
ID ADF30532 standard; protein; 2657 AA.
DE Mouse angiogenesis modulating protein #8.
PN US2003162706-A1.
PD 28-AUG-2003.
PA (PROCT & GAMBLE CO.
Query Match 10.8%; Score 378; DB 7; Length 2657;
Best Local Similarity 26.2%; Pred. No. 2.9e-23;
RESULT 1308
ID AAY13350 standard; protein; 915 AA.
DE Amino acid sequence of protein PRO219.
PN W09914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 2; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1309
ID AAY95340 standard; protein; 915 AA.
DE Human PRO219 antitumour protein.
PN W0200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 3; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1310
ID ADC78354 standard; protein; 915 AA.
DE Human PRO219 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 3; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1311
ID AAB80218 standard; protein; 915 AA.
DE Human PRO219 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1312
ID AAU12318 standard; protein; 915 AA.
DE Human PRO219 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1313

ID AAB53077 standard; protein; 915 AA.
DE Human angiogenesis-associated protein PRO219, SEQ ID NO:67.
PN WO20053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1314
ID ABU71596 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1315
ID ABO17762 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1316
ID ABU71451 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1317
ID ABU81016 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1318
ID ABU71897 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1319
ID ABO01780 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1320
ID ABU66716 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1321
ID ABU54353 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1322
ID ABO47368 standard; protein; 915 AA.

DE Human secreted/transmembrane polypeptide PRO219.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1323
ID ABU59797 standard; protein; 915 AA.
DE Novel secreted and transmembrane protein PRO219.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1324
ID ABO24987 standard; protein; 915 AA.
DE Human secreted/transmembrane protein (PRO) #147.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1325
ID ABU64505 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1326
ID ABU67351 standard; protein; 915 AA.
DE Human secreted protein PRO219.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1327
ID ABO14871 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1328
ID ABU66992 standard; protein; 915 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 294.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1329
ID ABU69628 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1330
ID ABO14810 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1331
ID ADA45613 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.

PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1332
ID ADA76244 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1333
ID ADB29239 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1334
ID ADA18894 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1335
ID ADA61517 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1336
ID ADB19302 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1337
ID ADB27843 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1338
ID ADA86322 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1339
ID ADB15886 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1340
ID ADA47672 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073215-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1341
ID ADA18095 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1342
ID ABO32762 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1343
ID ADA67467 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1344
ID ADB30474 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1345
ID ADA85770 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1346
ID ADA96982 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1347
ID ADA79286 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1348
ID ADA87425 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1349
ID ADB16627 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087349-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1350
ID ABO34822 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1351
ID ADA16070 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1352
ID ADA91719 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1353
ID ADA14782 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1354
ID ADA18743 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1355
ID ADA93958 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1356
ID ADA19854 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082891-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1357
ID ADB13166 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1358
ID ABO43295 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1359
ID ADA74420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1360
ID ADA42215 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1361
ID ADB24653 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1362
ID ADA82177 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1363
ID ADA75140 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1364
ID ADA85218 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1365
ID ADA84666 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1366
ID ABO17500 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1367
ID ADB29922 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1368
ID ABO43295 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1368
ID ADA80450 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1369
ID ADA75692 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1370
ID ADA46917 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1371
ID ADB25213 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1372
ID ADA93389 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1373
ID ADB26739 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1374
ID ADB31026 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1375
ID ADA60954 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1376
ID ADB24101 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1377
ID ADA96430 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1378
ID ADA81002 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1379
ID ADA95878 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1380
ID ADB26187 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1381
ID ADB21672 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 6; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1382
ID ADA77451 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1383
ID ADB18191 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1384
ID ADA86874 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1385
ID ADA16494 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1386
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ID ADA12923 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1387
ID ADA1791 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1388
ID ADA87977 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1389
ID ADA46365 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1390
ID ADA17138 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1391
ID ADA42641 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1392
ID ADB28395 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1393
ID ADB28947 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1394
ID ADA76699 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1395
ID ADA88529 standard; protein; 915 AA.

DE Novel human secreted and transmembrane protein PRO219.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1396
ID ADA97534 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1397
ID ADB27291 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1398
ID ADB22224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1399
ID ABO17561 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1400
ID ADA66915 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1401
ID ADB22776 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1402
ID ADB23549 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1403
ID ADA92271 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1404
ID ADB15334 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087352-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1405
ID ADB38586 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1406
ID ADB38034 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1407
ID ADB66506 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1408
ID ADB89586 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1409
ID ADB90318 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1410
ID ADB77560 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1411
ID ADB39419 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1412
ID ADB74696 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1413
ID ADB47042 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1414
ID ADB66649 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1415
ID ADB77254 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1416
ID ADB34411 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1417
ID ADB35515 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1418
ID ADB33859 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1419
ID ADB34963 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1420
ID ADB36067 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1421
ID ADB46462 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1422
ID ADC28342 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1423
ID ADC28342 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1423
ID ADC39542 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1424
ID ADC40056 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1425
ID ADC18864 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1426
ID ADC34180 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1427
ID ADC29235 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1428
ID ADC28766 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1429
ID ADC40651 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1430
ID ADC19308 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1431
ID ADC33756 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;

RESULT 1432
ID ADC12826 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1433
ID ADC50335 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1434
ID ADC71882 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1435
ID ADC59861 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1436
ID ADC52868 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1437
ID ADC57222 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1438
ID ADC60413 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1439
ID ADC50888 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1440
ID ADC65415 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1441

ID ADC54513 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1442
ID ADC53474 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1443
ID ADC58997 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1444
ID ADC55875 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1445
ID ADC58445 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1446
ID ADC12378 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1447
ID ADD03119 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1448
ID ADC90111 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1449
ID ADC69530 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1450
ID ADC48419 standard; protein; 915 AA.

DE Human PRO polypeptide #147.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1451
ID ADD09948 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1452
ID ADD04523 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1453
ID ADC80479 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1454
ID ADD10986 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1455
ID ADC47867 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1456
ID ADD04833 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1457
ID ADC79927 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1458
ID ADD09396 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1459
ID ADD03839 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.

PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1460
ID ADD03415 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1461
ID ADD41109 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1462
ID ADD52248 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1463
ID ADD52988 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1464
ID ADD53540 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1465
ID ADD51696 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1466
ID ADD02495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1467
ID ADD01929 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1468
ID ADD54111 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203432-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1469
ID ADD92428 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1470
ID ADD91324 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1471
ID ADD503938 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1472
ID ADD32235 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1473
ID ADE22167 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1474
ID ADD79391 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1475
ID ADE41927 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1476
ID ADE17744 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1477
ID ADD91876 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199053-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1478
ID ADE3339 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1479
ID ADE33891 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1480
ID ADD79943 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1481
ID ADD92980 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1482
ID ADE19400 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1483
ID ADE34667 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1484
ID ADE18848 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1485
ID ADE43044 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1486
ID ADD95833 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003198059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1487
ID ADE22719 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1488
ID ADD78837 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1489
ID ADE32787 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1490
ID ADE42479 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1491
ID ADD80495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1492
ID ADD89523 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1493
ID ADE40807 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1494
ID ADE04606 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1495
ID ADE92735 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1496
ID ADE92735 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1496
ID ADG21444 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1497
ID ADG23085 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1498
ID ADF97420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1499
ID ADG80484 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;
RESULT 1500
ID ADG79932 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.6%; Score 370; DB 7; Length 915;
Best Local Similarity 17.9%; Pred. No. 2.5e-23;

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